

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 22, 2005, 09:06:18 ; Search time 40 Seconds
(without alignments)
401.705 Million cell updates/sec

Title: US-10-617-955-2-COPY

Perfect score: 860
Sequence: 1 YSTEVEAAVNRLVNLVLRAS.....VKSAPAGLGEVLFERITLKHD 167

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: piri:.*
2: piri:.*
3: piri:.*
4: piri:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	839	97.6	175	1	FERHOL ferritin light cha
2	756	87.9	175	1	FERHOL ferritin light cha
3	745	86.6	175	2	feritin protein 1
4	738	85.8	175	2	feritin light cha
5	726	84.4	183	1	FERHOL ferritin light cha
6	724	84.2	183	2	feritin light cha
7	712	82.8	183	2	B33355 ferritin light cha
8	536	62.3	176	1	FERHOL ferritin, tadpole
9	535	62.2	176	2	A27805 ferritin chain H -
10	518	60.2	176	1	FERHOL ferritin heavy cha
11	513	59.7	176	1	C27805 ferritin chain M -
12	495	57.6	180	2	A26886 ferritin heavy cha
13	493	57.3	181	2	A39884 ferritin heavy cha
14	490	57.0	182	2	S06070 ferritin heavy cha
15	487	56.6	183	1	FERHOL ferritin heavy cha
16	481	55.9	164	2	I46710 ferritin heavy cha
17	463.5	53.9	174	2	S45603 ferritin, boma - g
18	457.5	53.2	174	2	B27805 ferritin chain L -
19	422.5	49.1	170	2	T33854 hypothetical prote
20	389.5	45.3	170	2	T31870 hypothetical prote
21	387.5	45.1	172	1	A45628 ferritin heavy cha
22	382	44.4	181	2	S62651 ferritin - signal
23	375.5	43.7	173	1	B45628 ferritin heavy cha
24	368	42.8	141	2	I48109 ferritin heavy cha
25	336	39.1	78	2	S06906 ferritin light cha
26	334.5	38.9	250	2	A40992 ferritin precursor
27	334.5	38.9	254	2	T08593 ferritin precursor
28	334.5	38.9	259	2	T47726 hypothetical prote
29	332	38.6	254	1	FERHOL ferritin heavy cha

30	332	38.6	256	2	T08123 ferritin 3 precurs
31	329.5	38.3	259	2	G84827 probable ferritin
32	324.5	37.7	250	2	T08124 ferritin 2 precurs
33	315.5	36.7	255	2	S71880 ferritin 1 precurs
34	315.5	36.7	285	2	S22498 ferritin 1 precurs
35	308	35.8	300	2	S24057 ferritin 2 precurs
36	295.5	34.4	253	2	S27358 ferritin precursor
37	242	28.1	80	2	S68315 ferritin H chain -
38	238	27.7	80	2	S06905 ferritin heavy cha
39	213	24.8	71	2	S06279 ferritin heavy cha
40	209	24.3	49	2	S68314 ferritin L chain -
41	196.5	22.8	239	2	S45604 ferritin precursor
42	175	20.3	43	2	S04979 ferritin light cha
43	169.5	19.7	164	2	E72293 ferritin - Thermot
44	148	17.2	171	2	G69077 ferritin like prot
45	142.5	16.6	229	2	S13978 aetemin - brine sh

ALIGNMENTS

RESULT 1

FERHOL ferritin light chain - horse

C:Species: Equus caballus (domestic horse)

C>Date: 11-Sep-1981 #sequence_revision 06-May-1998 #text_change 09-Jul-2004

C:Accession: S36118, A03267

R:Takeda, S.; Ohta, M.; Ebina, S.; Nagayama, K.

Biochim. Biophys. Acta 1174, 218-220, 1993

A:Title: Cloning, expression and characterization of horse L-ferritin in Escherichia coli

A:Reference number: S36118; PMID:93363645; PMID:8357841

A:Accession: S36118

A:Molecule type: mRNA

A:Residues: 1-175 <TAK>

A:Cross-references: UNIPROT:P02791; GB:D14523; NID:9406208; PIDN:BAA03396.1; PID:9406209

A:Experimental source: liver

R:Heusterspreute, M.; Crichton, R.R.

FEBS Lett. 129, 322-327, 1981

A:Title: Amino acid sequence of horse spleen apoferritin.

A:Reference number: A91294; PMID:82027739; PMID:7026284

A:Accession: A03267

A:Molecule type: protein

A:Residues: 2-93, 11, 95-175 <HEU>

A:Experimental source: spleen

R:Stegsy, G.A.; Stansfield, R.F.D.; Bourne, P.E.; Harrison, P.M.

Nature 288, 298-300, 1980

A:Title: Helix packing and subunit conformation in horse spleen apoferritin.

A:Reference number: A93239; PMID:81052459; PMID:7432529

A:Contents: annotation: X-ray crystallography, 2.8 angstroms

C:Comment: Ferritin is an intracellular molecule that stores iron in a soluble, nontoxic

form in a central cavity in which the polymeric ferric iron core is deposited.

C:Comment: There are two types of ferritin subunits: L (light) chain and H (heavy) chain

C:Comment: In horse spleen the light chain is the major chain.

C:Superfamily: ferritin

C:Keywords: acetylated amino end; iron; iron storage; liver; metalloprotein; multimer; s

F/2-175/Product: ferritin light chain #status experimental <MAT>

F/2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental

F/54,57,58,61,64/Binding site: iron (Glu) #status predicted

Query Match 97.6% Score 839; DB 1; Length 175;
Best Local Similarity 97.6% Pred. No. 7,1e-64;
Matches 163; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY	1	YSTEVEAAVNRLVNLVLRASYYSLGTFPDDVALGCVCFPRFLAEKKEGAEIRLLK 60
DB	9	YSTEVEAAVNRLVNLVLRASYYSLGTFPDDVALGCVCFPRFLAEKKEGAEIRLLK 68
QY	61	MONORGGRALPDOLKPSODEWGCTPDAMKAIIVEKSNQALDIALGSKKADPHLCD 120
DB	69	MONORGGRALPDOLKPSODEWGCTPDAMKAIIVEKSNQALDIALGSKKADPHLCD 128
QY	121	FLSHFDDEVYLIKKMGDHLNTIQLVYKSKGLGEVLFERITLKHD 167

Nucleic Acids Res. 16, 7741, 1988
A>Title: Nucleotide sequence of cDNA encoding rabbit ferritin L chain.

A;Reference number: S01239; MUID:88319979; PMID:3412911
A;Accession: S01239

A;Molecule type: mRNA
A;Residues: 1-175 <DNA>

A;Cross-references: UNIPROT:P09451; EMBL:X07630; NID:g1558; PIDN:CAA30682.1; PID:g1559
C;Superfamily: ferritin

Query Match 85.8%; Score 738; DB 2; Length 175;
Best Local Similarity 85.6%; Pred. No. 2.5e-55;
Matches 143; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

OY 1 YSTEVEAAVNRLVNLVLRASYYTLISGFYFDRDDVALGCVHFFRELAEBKREGAERLLK 60
DB 9 YSPEVEAAVNRLVNLVLRASYYTLISGFYFDRDDVALGCVHFFRELAEBKREGAERLLK 68
OY 61 MONORGGRAFLFODLQKPSQDEWGTTPDAMKAAIVLEKSLNQALDLDHALGSKKADPHLCD 120
DB 69 MONORGGRAFLFODVQKPSQDEWGTTPDAMKAAIVLEKSLNQALDLDHALGSKKADPHLCD 128
OY 121 FLESHFLDEEYVLLIKKMGDHLTNIRLVSKAGLGYLPERLTLLKHD 167
DB 129 FLESHFLDEEYVLLIKKMGDHLTNIRLVSKAGLGYLPERLTLLKHD 175

RESULT 5

FRRTL
ferritin light chain - rat

C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Aug-1985 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004

C;Accession: A29575; A03268
R;Leibold, B.A.; Aaliz, N.; Brown, A.J.P.; Munro, H.N.

J. Biol. Chem. 262, 7335-7341, 1987

A>Title: Characterization and evolution of the expressed rat ferritin light subunit gene
A;Reference number: A29575; MUID:87222340; PMID:3584116

A;Accession: A29575
A;Molecule type: DNA

A;Residues: 1-183 <LEI>
A;Cross-references: UNIPROT:P02793; GB:J02741; NID:G204132; PIDN:AAA41152.1; PID:G204133

R;Leibold, B.A.; Aaliz, N.; Brown, A.J.P.; Munro, H.N.

J. Biol. Chem. 259, 4327-4334, 1984

A>Title: Conservation in rat liver of light and heavy subunit sequences of mammalian fer

A;Reference number: A2474; MUID:84162134; PMID:6546756

A;Accession: A03268
A;Molecule type: mRNA

A;Residues: 2-97, 'K', '99-120, 'OA', '123-154, 'W', '156-183 <LE2>
A;Cross-references: GB:K01930; NID:G204130; PIDN:AAA41154.1; PID:G204131

A;Note: Initiator Met not shown
C;Comment: This ferritin mRNA was isolated from liver parenchymal cells.

C;Comment: The rat light chain has an octapeptide insertion after residue 158 compared w

C;Comment: ferritin is an intracellular molecule that stores iron in a soluble, nontoxic

C;Comment: ferritin in which the polymeric ferric iron core is deposited.

C;Comment: There are two types of ferritin subunits: L (light) chain and H (heavy) chain

C;Superfamily: ferritin
C;Keywords: iron storage; liver; multimer

Query Match 84.4%; Score 726; DB 1; Length 183;
Best Local Similarity 80.6%; Pred. No. 2.7e-54;
Matches 141; Conservative 17; Mismatches 9; Indels 8; Gaps 1;

OY 1 YSTEVEAAVNRLVNLVLRASYYTLISGFYFDRDDVALGCVHFFRELAEBKREGAERLLK 60
DB 9 YSPEVEAAVNRLVNLVLRASYYTLISGFYFDRDDVALGCVHFFRELAEBKREGAERLLK 68
OY 61 MONORGGRAFLFODLQKPSQDEWGTTPDAMKAAIVLEKSLNQALDLDHALGSKKADPHLCD 120
DB 69 MONORGGRAFLFODVQKPSQDEWGTTPDAMKAAIVLEKSLNQALDLDHALGSKKADPHLCD 128
OY 121 FLESHFLDEEYVLLIKKMGDHLTNIRLVSKAGLGYLPERLTLLKHD 167
DB 129 FLESHFLDEEYVLLIKKMGDHLTNIRLVSKAGLGYLPERLTLLKHD 183

RESULT 6
154774
ferritin light chain - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: 154774
R;Denlis, M.G.

Int. J. Cancer 50, 930-936, 1992

A>Title: Isolation of cDNA clones corresponding to genes differentially expressed in two

A;Reference number: 154774; MUID:92210224; PMID:1555892

A;Accession: 154774
A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA
A;Residues: 1-183 <RES>
A;Cross-references: UNIPROT:P02793; GB:L01122; NID:G204122; PIDN:AAA41152.1; PID:G204123

C;Superfamily: ferritin

Query Match 84.2%; Score 724; DB 2; Length 183;
Best Local Similarity 80.0%; Pred. No. 4e-54;
Matches 140; Conservative 17; Mismatches 10; Indels 8; Gaps 1;

OY 1 YSTEVEAAVNRLVNLVLRASYYTLISGFYFDRDDVALGCVHFFRELAEBKREGAERLLK 60
DB 9 YSPEVEAAVNRLVNLVLRASYYTLISGFYFDRDDVALGCVHFFRELAEBKREGAERLLK 68
OY 61 MONORGGRAFLFODLQKPSQDEWGTTPDAMKAAIVLEKSLNQALDLDHALGSKKADPHLCD 120
DB 69 MONORGGRAFLFODVQKPSQDEWGTTPDAMKAAIVLEKSLNQALDLDHALGSKKADPHLCD 128
OY 121 FLESHFLDEEYVLLIKKMGDHLTNIRLVSKAGLGYLPERLTLLKHD 167
DB 129 FLESHFLDEEYVLLIKKMGDHLTNIRLVSKAGLGYLPERLTLLKHD 183

RESULT 7

B33355
ferritin light chain - mouse

C;Species: Mus musculus (house mouse)
C;Date: 20-Dec-1989 #sequence_revision 20-Dec-1989 #text_change 09-Jul-2004

C;Accession: B33355
R;Beaumont, C.; Dugast, I.; Renaudie, F.; Souroujon, M.; Grandchamp, B.

J. Biol. Chem. 264, 7498-7504, 1989

A>Title: Transcriptional regulation of ferritin H and L subunits in adult erythroid and

ferritin shells.
A;Reference number: A33355; MUID:89214195; PMID:2708374

A;Accession: B33355
A;Status: preliminary

A;Molecule type: mRNA
A;Residues: 1-183 <BEA>
A;Cross-references: UNIPROT:P29391; GB:J04716; NID:G193268; PIDN:AAA37614.1; PID:G30234

C;Superfamily: ferritin

Query Match 82.8%; Score 712; DB 2; Length 183;
Best Local Similarity 78.3%; Pred. No. 4.1e-53;
Matches 137; Conservative 17; Mismatches 13; Indels 8; Gaps 1;

OY 1 YSTEVEAAVNRLVNLVLRASYYTLISGFYFDRDDVALGCVHFFRELAEBKREGAERLLK 60
DB 9 YSPEVEAAVNRLVNLVLRASYYTLISGFYFDRDDVALGCVHFFRELAEBKREGAERLLK 68
OY 61 MONORGGRAFLFODLQKPSQDEWGTTPDAMKAAIVLEKSLNQALDLDHALGSKKADPHLCD 120
DB 69 MONORGGRAFLFODVQKPSQDEWGTTPDAMKAAIVLEKSLNQALDLDHALGSKKADPHLCD 128
OY 121 FLESHFLDEEYVLLIKKMGDHLTNIRLVSKAGLGYLPERLTLLKHD 167
DB 129 FLESHFLDEEYVLLIKKMGDHLTNIRLVSKAGLGYLPERLTLLKHD 183

RESULT 8

FRRGL

ferritin, tadpole - bullfrog
C:Species: Rana catesbeiana (bullfrog)
C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
C:Accession: A25627
R:Didabury, J.R.; Theill, E.C.; Kaufman, R.E.; Dickey, L.F.
J: Biol. Chem. 261, 949-955, 1986
A:Title: Multiple red cell ferritin mRNAs, which code for an abundant protein in the emb
A:Reference number: A25627; MUID:86085540; PMID:3484480
A:Accession: A25627
A:Molecule type: mRNA
A:Residues: 1-176 <DID>
A:Cross-references: UNIPROT:P07229; GB:M1210; NID:g213691; PIDN:AAA49532.1; PID:g213692
A:Experimental source: reticulocytes
C:Comment: The sequence of this ferritin is more similar to mammalian H chains than to I
C:Superfamily: ferritin
C:Keywords: erythrocyte, iron storage

Query Match 62.3%; Score 536; DB 1; Length 176;
Best Local Similarity 58.5%; Pred. No. 3e-38;
Matches 96; Conservative 38; Mismatches 30; Indels 0; Gaps 0;

QY 1 YSTEVEAAVNLVNLVYASTYTLISLGFYFDRDVALRGVCFPRELAEEKREGAERLLK 60
DB 9 FHRDCEAIIHNVMMELIYASTYLSMAFYFDRDIALHNVAKFPKQSHERRHAETKLM 68
61 MÖNÖRGGAALQODLOKPSQDEWGTTTPDAMKAATVLEKSLNALDLDHALGSKKADPHLCD 120
DB 69 DÖNKRGGGIVIVADYKPERDEMGNTLEAMQALDLEKTVNALDLDLHKVGSDDKVDPHLCD 128
121 FLESHFLDEEYKLIKKMGDHLTNIOQLVKSAGAGEYLFERLT 164
DB 129 FLEETYLEÖVKSIIKÖLGDYITNLKRLGLPÖNGEGEYLFDKHTM 172

RESULT 9
A27805
ferritin chain H - bullfrog
C:Species: Rana catesbeiana (bullfrog)
C:Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 09-Jul-2004
C:Accession: A27805
R:Dickey, L.F.; Sreedharan, S.; Theill, E.C.; Didabury, J.R.; Wang, Y.H.; Kaufman, R.E.
J: Biol. Chem. 262, 7901-7907, 1987
A:Title: Differences in the regulation of messenger RNA for housekeeping and specialized
nification of the first processed pseudogene in amphibia.
A:Reference number: A92648; MUID:8722424; PMID:3495534
A:Accession: A27805
A:Molecule type: mRNA
A:Residues: 1-176 <DID>
A:Cross-references: UNIPROT:P07229; GB:M15655; NID:g213672; PIDN:AAA49523.1; PID:g213673
C:Superfamily: ferritin

Query Match 62.2%; Score 535; DB 2; Length 176;
Best Local Similarity 58.5%; Pred. No. 3.6e-38;
Matches 96; Conservative 38; Mismatches 30; Indels 0; Gaps 0;

QY 1 YSTEVEAAVNLVNLVYASTYTLISLGFYFDRDVALRGVCFPRELAEEKREGAERLLK 60
DB 9 FHRDCEAIIHNVMMELIYASTYLSMAFYFDRDIALHNVAKFPKQSHERRHAETKLM 68
61 MÖNÖRGGAALQODLOKPSQDEWGTTTPDAMKAATVLEKSLNALDLDHALGSKKADPHLCD 120
DB 69 DÖNKRGGGIVIVADYKPERDEMGNTLEAMQALDLEKTVNALDLDLHKVGSDDKVDPHLCD 128
121 FLESHFLDEEYKLIKKMGDHLTNIOQLVKSAGAGEYLFERLT 164
DB 129 FLEETYLEÖVKSIIKÖLGDYITNLKRLGLPÖNGEGEYLFDKHTM 172

RESULT 10
FRXL
ferritin heavy chain - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 30-Sep-1991 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004

C:Accession: A37959; S12463; S09499; A40408
 R.Holland, L.J.; Mall, A.A.; Bhattacharya, A.
 Biochemistry 30, 1965-1972, 1991
 A>Title: Xenopus liver ferritin H subunit; cDNA sequence and mRNA production in the liver
 A:Reference number: A37959; MUID:91129281; PMID:1993207
 A:Accession: A37959
 A:Molecule type: mRNA
 A:Residues: 1-176 <HOL>
 A:Cross-references: UNIPROT:P17663; GB:M55010; NID:g214135; PIDN:AAA49708.1; PID:g214136
 A:Experimental source: liver
 R.Schoenberg, D.
 submitted to the EMBL Data Library, January 1990
 A:Reference number: S12463
 A:Accession: S12463
 A:Molecule type: mRNA
 A:Residues: 1-5, 'L', '7-14', 'I', '16-156', 'A', '159-176' <SCH>
 A:Cross-references: EMBL:X51395; NID:g64690; PIDN:CMAA5760.1; PID:g64691
 R.Moskatis, J.E.; Pascorì, R.L.; Schoenberg, D.R.
 Nucleic Acids Res. 18, 2184, 1990
 A>Title: Sequence of Xenopus laevis ferritin mRNA.
 A:Reference number: S09499; MUID:90245677; PMID:2336402
 A:Accession: S09499
 A:Molecule type: mRNA
 A:Residues: 1-5, 'L', '7-14', 'I', '16-64', '70-86', 'KFLKY', '87-156', 'A', '159-176' <MOS>
 A:Cross-references: EMBL:X51395
 A>Note: the sequence shown in the alignment is inconsistent with the nucleotide sequence
 R.Muller, U.P.; Vedel, M.; Monnot, M.J.; Touzet, N.; Wegnez, M.
 DNA Cell Biol. 10, 571-579, 1991
 A>Title: Molecular cloning and expression of ferritin mRNA in heavy metal-poisoned Xenopus
 A:Reference number: A40408; MUID:92029619; PMID:1718317
 A:Accession: A40408
 A:Molecule type: mRNA
 A:Residues: 1-9, 'H', '11-22', 'W', '24-90', 'G', '92-96', 'T', '98-123', 'AH', '126-143', 'Q', '145-176' <MU>
 A:Cross-references: EMBL:X64727
 A:Experimental source: cadmium-poisoned XL2 embryonic cell line
 C:Complex: The functional molecule is composed of 24 chains, is roughly spherical and con-
 C:Function:
 A:Description: intracellular protein that stores and transports iron in a soluble, nontox-
 C:Superfamily: ferritin
 C:Keywords: iron; iron binding; iron storage; iron transport; metalloprotein; multimer
 F:24,58,59,61,62,104/Binding site: iron (Glu, Glu, Glu, Glu, His, Glu) #status predicted
 F:83/Binding site: iron (Asp) (shared with tetrameric partners) #status predicted
 F:83/Binding site: iron (Lys) (shared with tetrameric partners) #status predicted

A:Accession: S01948
A:Molecule type: mRNA
A:Residues: 1-182 <MT>
A:Cross-references: EMBL:X1812; NID:G50951; PIDD:CAA31300.1; PID:G50952
R:Torci, S.V.; Kwak, E.L.; Miller, S.C.; Miller, L.L.; Ringold, G.M.; Myambo, K.B.; Young
J. Biol. Chem. 263, 12638-12644, 1988
A:Title: The molecular cloning and characterization of murine ferritin heavy chain, a tu
A:Reference number: A31113; MUID:88315064; PMID:3410854
A:Accession: A31113
A:Molecule type: mRNA
A:Residues: 1-182 <TOR>
A:Cross-references: GB:J03941; NID:G193264; PIDD:AAA37611.1; PID:G309232
R:Beaumont, C.; Dugaes, I.; Renaudie, F.; Souroujon, M.; Grandchamp, B.
J. Biol. Chem. 264, 7498-7504, 1989
A:Title: Transcriptional regulation of ferritin H and L subunits in adult erythroid and
ferritin shells.
A:Reference number: A33355; MUID:89214195; PMID:2708374
A:Accession: A33355
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-16, 'S', 18-136, 'H', 138-139, 'N', 141-163, 'S', 165-182 <BEA>
A:Cross-references: GB:M4509; NID:G193266; PIDD:AAA37612.1; PID:G309233
A:Note: the protein sequence from Fig. 2 is inconsistent with the nucleotide sequence fr
d 164
C:Genetics:
A:Supfam: 38/3, 87/3, 129/3
C:Superfamily: ferritin

Query Match 57.0%; Score 490; DB 2; Length 182;
Best Local Similarity 53.0%; Pred. No. 2.4e-34;
Matches 88; Conservative 39; Mismatches 39; Indels 0; Gaps 0;

QY 1 YSTEVEAAVNLVNLVLYLRASYTYLSLGFYPDRDDVALRGVCHFRELAEEKREGAERLLK 60
Db 13 YHQAEAAINQINQINELVASYVYLMSCTFPRDDVALKNFAKVFYHQSHERRHAKLTK 72
QY 61 MONRGGRALFODLOKQSDQEWGTTTPDAMKAALVLEKSLNALDIALGSKKADPHLCD 120
Db 73 LQNGRGGRIFLQDIDIKKPPDRDWESGLNAMECALHLEKSVNOSLLEHLATDKNDPHLCD 132
QY 121 FLESHFLDEEYKLTKKMGDHLTNIORLVKSNAGSEYLFERLTLLKH 166
Db 133 FLETYLSQVKSILELGDHVTNLKMGAPRAGMAEYLFDKHTLGH 178

RESULT 15

FRHH

N:Alternate names: apoferritin H; ferritin heavy polypeptide 1
C:Species: Homo sapiens (man)
C:Date: 28-Aug-1985 #sequence revision 31-Dec-1993 #text change 09-Jul-2004
R:Costanzo, F.; Colombo, M.; Staemfeli, S.; Sanctoro, C.; Marone, M.; Frank, R.; Dellus,
Nucleic Acids Res. 14, 721-736, 1986
A:Title: Structure of gene and pseudogenes of human apoferritin H.
A:Reference number: A23517; MUID:86120367; PMID:3003694
A:Accession: A23517
A:Molecule type: DNA
A:Residues: 1-183 <COS>
A:Cross-references: UNIPROT:P02194; GB:X03487; NID:G31340; PIDD:CAA27205.1; PID:G762940.
R:Heintze, M.W.; Keim, S.; Papadopoulos, P.; O'Brien, S.; Modi, W.; Drysdale, J.; Leonard
Proc. Natl. Acad. Sci. U.S.A. 83, 7226-7230, 1986
A:Title: Cloning, characterization, expression, and chromosomal localization of a human
A:Reference number: A25045; MUID:87016920; PMID:3020541
A:Accession: A25045
A:Molecule type: DNA
A:Residues: 1-183 <HEN>
A:Cross-references: GB:M14211; GB:M14212; NID:G182509; PIDD:AAA52438.1; PID:G182511; GB:
R:Bar, M.; Chauthaiwale, V.; Joshi, J.G.
Gene 126, 275-278, 1993
A:Title: Sequence of a cDNA encoding the ferritin H-chain from an 11-week-old human fetus
A:Reference number: JN0571; MUID:93246257; PMID:7916709
A:Accession: JN0571

```

A:Molecule type: mRNA
A:Residues: 1-183 <DBA>
A:Cross-references: GDB:M9716; NID:g306743; PIDDN:AAA5892.1; PID:g306744
R:Boyd, D.; Vecoli, C.; Belcher, D.M.; Jain, S.K.; Drysdale, J.M.
J. Biol. Chem. 260, 11755-11761, 1985
A:Title: Structural and functional relationships of human ferritin H and L chains deduced
A:Reference number: A92494; MUID:86008223; PMID:3840162
A:Accession: A23920
A:Molecule type: mRNA
A:Residues: 1-183 <BOY>
A:Cross-references: GDB:M11146; NID:g182504; PIDDN:AAA52437.1; PID:g182505
R:Chou, C.C.; Gatti, R.A.; Fuller, M.L.; Concannon, P.; Wong, A.; Chada, S.; Davis, R.C.,
Mol. Cell. Biol. 6, 566-573, 1986
A:Title: Structure and expression of ferritin genes in a human promyelocytic cell line ct
A:Reference number: A93087; MUID:87064341; PMID:3023856
A:Accession: A2484
A:Molecule type: mRNA
A:Residues: 1-183 <CHO>
A:Cross-references: GDB:M12937; NID:g182506; PIDDN:AAA5830.1; PID:g182507
A:Note: The authors translated the codon CAG for residue 113 as Glu
R:Costanzo, P.; Santoro, C.; Colantuoni, V.; Bensl, G.; Rangeli, G.; Romano, V.; Cortese,
EMBO J. 3, 23-27, 1984
A:Title: Cloning and sequencing of a full length cDNA coding for a human apoferritin H ct
A:Reference number: A03269; MUID:84158535; PMID:6323167
A:Accession: A03269
A:Molecule type: mRNA
A:Residues: 1-175, 'WRVIMKAPRANP', <CO2>
A:Cross-references: GDB:X00318; NID:g28434; PIDDN:CAA25086.1; PID:g28435
A:Note: This sequence has been revised in reference A23517
R:Linzagro, A.; Felici, F.; Tramontano, A.; Pessi, A.; Cortese, R.
Gene 128, 51-57, 1993
A:Title: Mimicking of discontinuous epitopes by phage-displayed peptides, I. Epitope map
A:Reference number: P00563; MUID:93285469; PMID:7685501
A:Contents: annotation; artificial epitopes
R:Lawson, D.M.; Artymkuk, P.J.; Yewdall, S.J.; Smith, J.M.A.; Livingstone, J.C.; Trefry,
Nature 349, 541-544, 1991
A:Title: Solving the structure of human H ferritin by genetically engineering intermolecu
A:Reference number: A57130; MUID:91125486; PMID:1992356
A:Contents: annotation; X-ray crystallography, 2.4 angstroms, residues 6-86, 'Q', 88-177
C:Comment: There are several distinct binding sites for iron. Two sites each consist of t
ay bind several iron atoms and possess ferroxidase activity.
C:Genetics:
A:Gene: GDB:FTM1; FTHL6
A:Cross-references: GDB:120617; OMIM:134770
A:Map position: 11q12-11q13
A:Introns: 38/3; 87/3; 129/3
C:Complex: the functional molecule, composed of 24 chains, is roughly spherical with a ce
(H) chain and light (L) chain (see PIR:FEHUL). The predominant chain can be light or hea
C:Function:
A:Description: intracellular protein that stores and transports iron in a soluble, nontox
A:Note: tissues containing high levels of iron and involved in long-term storage tend to
C:Superfamily: ferritin
C:Keywords: iron; iron binding; iron storage; iron transport; metalloprotein; multimer
F:28, 62, 63, 65, 66, 108/binding site: iron (Glu, Glu, Glu, Glu, His, Glu) #status predicted
F:85/binding site: iron (Asp) (shared with tetrameric partners) #status experimental
F:87/binding site: iron (Lys) (shared with tetrameric partners) #status experimental

```

Tue Aug 23 10:27:26 2005

us-10-617-955-2-copy.rpr

Page 7

Search completed: August 22, 2005, 09:10:52
Job time : 41 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 22, 2005, 09:06:17 ; Search time 42 Seconds
(without alignments)
296.819 Million cell updates/sec

Title: US-10-617-955-2-COPY

Perfect score: 860
Sequence: 1 YSTEVEAAVNRLVNLVLRAS.....VKSAGLGEYLPERLTAKHD 167

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCUTS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	756	87.9	175	4	US-09-919-039-333
2	731	85.0	238	4	US-09-949-016-10295
3	487	56.6	220	4	US-09-949-016-10773
4	334	38.8	250	4	US-09-918-830-2
5	334	38.8	250	4	US-09-918-830-3
6	256	29.8	243	2	US-08-829-110-3
7	221	25.7	107	4	US-09-621-976-4402
8	146	17.0	168	3	US-09-134-001C-4664
9	94	10.9	162	4	US-09-602-777A-8
10	88	10.2	175	4	US-09-489-039A-14335
11	83.5	9.7	644	3	US-09-300-909-18
12	82.5	9.6	168	4	US-09-543-681A-7822
13	82	9.5	998	4	US-09-198-452A-841
14	82	9.5	998	4	US-09-438-185A-793
15	80.5	9.4	629	3	US-09-300-909-19
16	80	9.3	277	4	US-09-602-777A-8
17	80	9.3	514	4	US-09-902-540-10406
18	79	9.2	719	4	US-09-763-902B-5
19	77.5	9.0	390	4	US-09-107-532A-6425
20	77.5	9.0	482	4	US-09-902-540-16249
21	77.5	9.0	502	4	US-09-949-016-7837
22	77	9.0	302	4	US-09-270-767-59138
23	77	9.0	501	4	US-09-270-767-59138
24	76.5	8.9	491	4	US-09-248-796A-19312
25	76	8.8	7831	4	US-09-902-540-12902
26	75	8.7	374	4	US-09-710-279-1562
27	75	8.7	397	3	US-09-134-001C-4104

28	75	8.7	610	4	US-09-252-991A-19594	Sequence 19594, A
29	74	8.6	397	4	US-09-252-991A-24798	Sequence 24798, A
30	74	8.6	3433	4	US-09-091-501B-10	Sequence 10, App1
31	74	8.6	3433	4	US-09-538-052-1136	Sequence 1136, Ap
32	73.5	8.5	163	4	US-09-489-039A-10135	Sequence 10135, A
33	73.5	8.5	173	3	US-08-818-112-82	Sequence 82, App1
34	73.5	8.5	173	3	US-08-818-112-83	Sequence 82, App1
35	73.5	8.5	173	3	US-09-056-556-82	Sequence 82, App1
36	73.5	8.5	173	4	US-09-072-967-82	Sequence 82, App1
37	73.5	8.5	181	4	US-09-050-739-54	Sequence 54, App1
38	73.5	8.5	181	4	US-09-489-039A-12447	Sequence 12447, A
39	73.5	8.5	208	4	US-09-252-991A-27913	Sequence 27913, A
40	73	8.5	314	4	US-09-902-540-10427	Sequence 10427, A
41	73	8.5	1074	4	US-09-902-540-16251	Sequence 16251, A
42	73	8.5	1114	4	US-08-002-202-13	Sequence 13, App1
43	72.5	8.4	414	1	US-08-002-202-17	Sequence 17, App1
44	72.5	8.4	414	1	US-08-002-202-19	Sequence 19, App1
45	72.5	8.4	414	1	US-08-002-202-19	Sequence 19, App1

ALIGNMENTS

RESULT 1
US-09-919-039-333
Sequence 333, Application US/09919039
Patent No. 6727066
GENERAL INFORMATION:
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
FILE REFERENCE: PA-0035 US
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 401
SOFTWARE: PERL Program
SEQ ID NO 333
LENGTH: 175
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6727066 4005778CD1
US-09-919-039-333

Query Match 87.9%; Score 756; DB 4; Length 175;
Best Local Similarity 86.2%; Pred. No. 9.6e-73;
Matches 144; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 YSTEVEAAVNRLVNLVLRAS...VKSAGLGEYLPERLTAKHD 60
DB 9 YSTEVEAAVNRLVNLVLRAS...VKSAGLGEYLPERLTAKHD 68
QY 61 MONORGRALPDODKPSODEGTPDAMKAAIVKESLNOALDLHALGSKADPHLCD 120
DB 69 MONORGRALPDODKPSODEGTPDAMKAAIVKESLNOALDLHALGSKADPHLCD 128
QY 121 FLESHFLDEEVLTKKMGDHLNLTQRLVKSAGLGEYLPERLTAKHD 167
DB 129 FLESHFLDEEVLTKKMGDHLNLTQRLVKSAGLGEYLPERLTAKHD 175

RESULT 2
US-09-949-016-10295
Sequence 10295, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYOMPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016

```

; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 10295
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10295
```

```

Query Match      85.0%; Score 731; DB 4; Length 238;
Best Local Similarity 84.3%; Pred. No. 6.8e-70;
Matches 140; Conservative 10; Mismatches 16; Indels 0; Gaps 0;
```

```

QY 1 YSTVEAAVNRVLNVLRYASVYTLISGFYPRDRDVALGVCCHPFEELAEKREGAERLLK 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 72 YSTDVEAAVNSIVNLYLDQSTYLSLGFYPRDRDVALGVCCHPFEELAEKREGAERLLK 131
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 MONORGRALFODLOKPSODEWGTTPDAMKAIVLEKSLNQALDIDHALGSKKADPHLCD 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 132 MONORGRALFODIKKPADEWGTTPDAMKAIVLEKSLNQALDIDHALGSKKADPHLCD 191
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 FLESHFLDEBYKLIKMGDHLTNLRIQRYKSKAGLGEYLPFRLLTKH 166
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 192 FLETHFLDEBYKLIKMGDHLTNLRIQRYKSKAGLGEYLPFRLLTKH 237
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```

RESULT 3
US-09-949-016-10773
; Sequence 10773, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 10773
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10773
```

```

Query Match      56.6%; Score 487; DB 4; Length 220;
Best Local Similarity 53.0%; Pred. No. 6.4e-44;
Matches 87; Conservative 40; Mismatches 37; Indels 0; Gaps 0;
```

```

QY 1 YSTVEAAVNRVLNVLRYASVYTLISGFYPRDRDVALGVCCHPFEELAEKREGAERLLK 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 50 YHDSAAVNRVLNVLRYASVYTLISGFYPRDRDVALGVCCHPFEELAEKREGAERLLK 109
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 MONORGRALFODLOKPSODEWGTTPDAMKAIVLEKSLNQALDIDHALGSKKADPHLCD 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 110 LONORGRALFODIKKPADEWGTTPDAMKAIVLEKSLNQALDIDHALGSKKADPHLCD 169
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 FLESHFLDEBYKLIKMGDHLTNLRIQRYKSKAGLGEYLPFRLLTKH 164
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 170 FLETHFLDEBYKLIKMGDHLTNLRIQRYKSKAGLGEYLPFRLLTKH 213
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```

RESULT 4
US-09-418-830-2
; Sequence 2, Application US/09418830
; Patent No. 6563019
; GENERAL INFORMATION:
; APPLICANT: Deak, Maria
; APPLICANT: Dudits, Dene
; APPLICANT: Torok, Karolyne
; APPLICANT: Saas, Laszlo
; APPLICANT: Barna, Balazs
; APPLICANT: Kiraly, Zoltan
; TITLE OF INVENTION: STRESS AND PATHOGEN RESISTANT PLANTS
; FILE REFERENCE: DEAK
; CURRENT APPLICATION NUMBER: US/09/418,830
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: HU 9700762
; PRIOR FILING DATE: 1997-04-16
; PRIOR APPLICATION NUMBER: HU 9700762
; PRIOR FILING DATE: 1997-09-22
; PRIOR APPLICATION NUMBER: HU 9700762
; PRIOR FILING DATE: 1998-03-09
; PRIOR APPLICATION NUMBER: PCT/GB98/01108
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Medicago sativa
US-09-418-830-2
```

```

Query Match      38.8%; Score 334; DB 4; Length 250;
Best Local Similarity 42.4%; Pred. No. 1.6e-27;
Matches 72; Conservative 38; Mismatches 52; Indels 8; Gaps 3;
```

```

QY 1 YSTVEAAVNRVLNVLRYASVYTLISGFYPRDRDVALGVCCHPFEELAEKREGAERLLK 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 85 YHDSAAVNRVLNVLRYASVYTLISGFYPRDRDVALGVCCHPFEELAEKREGAERLLK 144
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 MONORGRALFODLOKPSOD---EWGTPDAMKAIVLEKSLNQALDIDHALGSKKADPHLCD 116
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 145 YONIRGRVVLHPVSPSPFDEHAKGDALYAMELALSTKLVNKLNVHSVADRNDP 204
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 117 HLCDFLESHFLDEBYKLIKMGDHLTNLRIQRYKSKAGLGEYLPFRLLTKH 166
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 205 QLANFLESFLDEBYKLIKMGDHLTNLRIQRYKSKAGLGEYLPFRLLTKH 250
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```

RESULT 5
US-09-418-830-3
; Sequence 3, Application US/09418830
; Patent No. 6563019
; GENERAL INFORMATION:
; APPLICANT: Deak, Maria
; APPLICANT: Dudits, Dene
; APPLICANT: Torok, Karolyne
; APPLICANT: Saas, Laszlo
; APPLICANT: Barna, Balazs
; APPLICANT: Kiraly, Zoltan
; TITLE OF INVENTION: STRESS AND PATHOGEN RESISTANT PLANTS
; FILE REFERENCE: DEAK
; CURRENT APPLICATION NUMBER: US/09/418,830
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: HU 9700762
; PRIOR FILING DATE: 1997-04-16
; PRIOR APPLICATION NUMBER: HU 9700762
; PRIOR FILING DATE: 1997-09-22
; PRIOR APPLICATION NUMBER: HU 9700762
; PRIOR FILING DATE: 1998-03-09
; PRIOR APPLICATION NUMBER: PCT/GB98/01108
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 6
```

SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 3
 LENGTH: 250
 TYPE: PR1
 ORGANISM: Unknown Organism
 FEATURE: Description of Unknown Organism: we do not have
 OTHER INFORMATION: this information
 US-09-418-830-3

Query Match 38.8%; Score 334; DB 4; Length 250;
 Best Local Similarity 42.4%; Pred. No. 1.6e-27;
 Matches 72; Conservative 38; Mismatches 52; Indels 8; Gaps 3;

QY 1 YSTEVEAANRLVNLVLYRASYTYLSLGFYFDRDDVALGVCHEFFRELAEREKREGAERLLK 60
 DB 85 YQDEVESAINQINVENVSVYVHSLFAYFDRDVALGKAKFESESEEREHEKELMK 144
 QY 61 MONORGRALFQDLOKPSOD---EWGTPDMKKAIVLEKSLNQALLDLHALGSKKADP 116
 DB 145 YQNRIGRGVIVLPIVSPSEFPAHEKGDALYAMELALSLIEKLVNKKLVNHSVADRNNDP 204
 QY 117 HLCDFLESHFLDEEVKLIKMGDHLTNIQRLVKSAGLGEVLFERLTIKH 166
 DB 205 QLANFEEFIVEQVESIKKISEVYQLRVGK--GGVWHFDQ-TLLH 250

RESULT 6
 US-08-829-110-3
 Sequence 3, Application US/08829110
 Patent No. 5882890

GENERAL INFORMATION:
 APPLICANT: Hillman, Jennifer L.
 TITLE OF INVENTION: NOVEL REGULATORS OF G-PROTEIN
 TITLE OF INVENTION: SIGNALING
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/829,110
 FILING DATE: Filed Herewith
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:
 FILING DATE:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0259 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-845-0555
 TELEFAX: 415-845-4166
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 243 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: THYMOT02
 CLONE: 343504
 US-08-829-110-3

Query Match 29.8%; Score 256; DB 2; Length 243;
 Best Local Similarity 43.3%; Pred. No. 3.1e-19;
 Matches 71; Conservative 17; Mismatches 42; Indels 34; Gaps 7;

QY 1 YSTEVEAANRLVNLVLYRASYTYLSLGFYFDRDDVALGVCHEFFRELAEREKREGAERLLK 60
 DB 9 YSTEVEAANRLVNLVLYRASYTYLSLGFYFDRDDVALGVCHEFFRELAEREKREGAERLLK 63
 QY 61 MONORGRALFQDLOKPSOD---EWGTPDMKKAIVLEKSLNQALLDLHALGSKKADP 116
 DB 64 -----RASPEDAKPAMRPPSDIHSDSSSSSHQSLKSTAKMAASLENDLEDE--GV 114
 QY 112 KKADPHLCDFLESHFLDEEVKLIKMGDHLTNIQRLVKSAGLGEVLFERLTIKH 149
 DB 115 KR-----PREFLKEFSEENVLFWLACEDFKKMQDK-TOMQEKAK 153

RESULT 7
 US-09-621-976-4402
 Sequence 4402, Application US/09621976
 Patent No. 6639063

GENERAL INFORMATION:
 APPLICANT: Dumas Milne Edwards, J.B.
 APPLICANT: Jobert, S.
 TITLE OF INVENTION: ESTs and Encoded Human Proteins.
 FILE REFERENCE: GENSET.054PR2
 CURRENT APPLICATION NUMBER: US/09/621,976
 CURRENT FILING DATE: 2000-07-21
 NUMBER OF SEQ ID NOS: 19335
 SOFTWARE: Patent.pm
 SEQ ID NO 4402

LENGTH: 107
 TYPE: PR1
 ORGANISM: Homo sapiens
 US-09-621-976-4402

Query Match 25.7%; Score 221; DB 4; Length 107;
 Best Local Similarity 40.2%; Pred. No. 5.4e-16;
 Matches 43; Conservative 24; Mismatches 40; Indels 0; Gaps 0;

QY 26 LGFYFDRDDVALGVCHEFFRELAEREKREGAERLLKMONORGRALFQDLOKPSODEWGT 85
 DB 1 MAFYERDDVALGVCHEFFRELAEREKREGAERLLKMONORGRALFQDLOKPSODEWGT 60
 QY 86 PDAMKAIVLEKSLNQALLDLHALGSKKADPHLCDFLESHFLDEEVK 132
 DB 61 LEAMECAHLEKSTIVSLIEHLQALALEKGEPSCATSWRATTLHQVK 107

RESULT 8
 US-09-134-001C-4664
 Sequence 4664, Application US/09134001C
 Patent No. 6380370

GENERAL INFORMATION:
 APPLICANT: Lynn Doucetle-Stamm et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: GTC-007
 CURRENT APPLICATION NUMBER: US/09/134,001C
 CURRENT FILING DATE: 1998-08-13
 PRIOR APPLICATION NUMBER: US 60/064,964
 PRIOR FILING DATE: 1997-11-08
 PRIOR APPLICATION NUMBER: US 60/055,779
 PRIOR FILING DATE: 1997-08-14
 NUMBER OF SEQ ID NOS: 5674
 SEQ ID NO 4664

LENGTH: 168
 TYPE: PR1
 ORGANISM: Staphylococcus epidermidis
 US-09-134-001C-4664

```

      PRIOR FILING DATE: 1999-08-31
      PRIOR APPLICATION NUMBER: DE 19941379.7
      PRIOR FILING DATE: 1999-08-31
      PRIOR APPLICATION NUMBER: DE 19941390.8
      PRIOR FILING DATE: 1999-08-31
      PRIOR APPLICATION NUMBER: DE 19941391.6
      PRIOR FILING DATE: 1999-08-31
      PRIOR APPLICATION NUMBER: DE 19942088.2
      PRIOR FILING DATE: 1999-09-03
      NUMBER OF SEQ ID NOS: 442
      SEQ ID NO 362
      LENGTH: 162
      TYPE: PRT
      ORGANISM: Corynebacterium glutamicum
      US-09-602-777A-362

      Query Match      10.9%; Score 94; DB 4; Length 162;
      Best Local Similarity 22.1%; Pred. No. 0.034;
      Matches 34; Conservative 38; Mismatches 72; Indels 10; Gaps 4;

      QY      4 EVEAAVNRVLNVLIRASTYTLISLGFYPRDDVALLEGVCHFFPELAEKREGABRLLKMQN 63
      DB      6 KIASFNNQVTAELFASWVYLQLSYVL--DDLGLTGMDDMKMAQSKBELHAKTPAQHLL 63
      QY      64 ORGGRALFQDLQKPSQDEWGTTPDAMKAIVLEKSLNOALLDIALGSKAD---PHLCD 120
      DB      64 DRDTYTPQIGDIAPPLDVTSAI-EAFESLAEQKISGIRLELAIQDAEKYDGRALID 122
      QY      121 FLESHFLDEEVKLIKMGDHLTNIQRLVYSKAGL 154
      DB      123 W----FLNEQIEBEATVGEIIDRLRLIADDSGSGI 152

      RESULT 10
      US-09-489-039A-14335
      Sequence 14335, Application US/09489039A
      Patent No. 6610836
      GENERAL INFORMATION:
      APPLICANT: Gary Breton et. al
      TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
      TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
      FILE REFERENCE: 2709.2004001
      CURRENT APPLICATION NUMBER: US/09/489,039A
      CURRENT FILING DATE: 2000-01-27
      PRIOR APPLICATION NUMBER: US 60/117,747
      PRIOR FILING DATE: 1999-01-29
      NUMBER OF SEQ ID NOS: 14342
      SEQ ID NO 14335
      LENGTH: 175
      TYPE: PRT
      ORGANISM: Klebsiella pneumoniae
      US-09-489-039A-14335

      Query Match      10.2%; Score 88; DB 4; Length 175;
      Best Local Similarity 22.4%; Pred. No. 0.16;
      Matches 36; Conservative 29; Mismatches 86; Indels 10; Gaps 4;

      QY      3 TEVAAVNRVLNVLIRASTYTLISLGFYPRDDVALLEGVCHFFPELAEKREGABRLLKMQ 62
      DB      14 TDMIDKINEQNLIELYSLLVQQMSAWCSYH--SPEGAAAFRRHAQSEMTMQRLFDYL 71
      QY      63 NORGGRALFQDLQKPSQDEWGTTPDAMKAIVLEKSLNOALLDIALGSKADPHLCDPL 122
      DB      72 TDTGSLPRLINAIASFFA-EVASLDELFRQTYHEHGLITQKINELHAAMTSODYPTFNPL 130
      QY      123 ESHFLD--EEVKLIKMGDHLTNIQRLVYSKAGLEAYLFEER 161
      DB      131 QWYVAQHEEKEKLFEKSVIDKLT----LAGSGGBGLYFIDK 166

      RESULT 11
      US-09-300-909-18
      Sequence 18, Application US/09300909

```

Patent No. 6306580
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: PREPARATION OF HUMAN PAPILLOMAVIRUS E1 HAVING
TITLE OF INVENTION: HELICASE ACTIVITY AND METHOD THEREFOR
NUMBER OF SEQUENCES: 27
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA: US/09/300,509
APPLICATION NUMBER: US/09/300,509
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/083,942
FILING DATE: 01-MAY-1998
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 644 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-300-909-18

Query Match 9.7%; Score 83.5; DB 3; Length 644;
Best Local Similarity 21.9%; Pred. No. 3;
Matches 28; Conservative 22; Mismatches 55; Indels 23; Gaps 2;

QY 60 KMNQGRGALFQDLQPSQDEWGTTPDAMKAIVLEKSLNALDLHLSKKAADPHIC 119
DB 304 KLRSGTCALYWRMTAMSNISDVQGTTPPEWIDRLTYLQHSFNINIDLSHMVQWADNBLT 363
QY 120 D-----FLSHFLDEEVKLIKMGMDHLTNIORLTKSRAGGEYLF 159
DB 364 DSDSIAYYQAQADNSNAAPFLKS--NSQAKIVDCGIMCRHYKKAERKMSIGQMIQ 420
QY 160 ERLTLKH 167
DB 421 SRCEKTND 428

RESULT 12
US-09-543-681A-7822
Sequence 7822, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 7822
LENGTH: 168
TYPE: PRT
ORGANISM: Proteus mirabilis
US-09-543-681A-7822

Query Match 9.6%; Score 82.5; DB 4; Length 168;
Best Local Similarity 23.2%; Pred. No. 0.6; DB 4; Length 168;
Matches 32; Conservative 24; Mismatches 77; Indels 5; Gaps 3;

QY 9 VNRVLVLYRASVYLSLGFYDPDVALEGVCHFRRLAEKREGAERLLKMNQGRGR 68
DB 11 LNRQLLLEFYSANLYQMSAMC--DDKGFDAKFLKASRBEHEMQRLLFDYLSPTGAM 68
QY 69 ALFQDLQPSQDEWGTTPDAMKAIVLEKSLNALDLHLSKKAADPHICPLBSHFID 128

DB 69 PLGTIEAPPA-EFLSLSDLFTKTYEHEKFTIAEINKLHIAMTQDYSFENFLQWYVAE 127
QY 129 --EEVKLIKMGDHLTNI 144
DB 128 QHEEKLFKSLIDKLAMV 145

RESULT 13
US-09-198-452A-841
Sequence 841, Application US/09198452A
Patent No. 6559294
GENERAL INFORMATION:
APPLICANT: Griffeis, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 841
LENGTH: 998
TYPE: PRT
ORGANISM: Chlamydia pneumoniae
US-09-198-452A-841

Query Match 9.5%; Score 82; DB 4; Length 998;
Best Local Similarity 24.1%; Pred. No. 7.9;
Matches 34; Conservative 17; Mismatches 50; Indels 40; Gaps 5;

QY 12 LVNLYLRASVYLSLGF---YEDRDDVA-----LGVCHFRRLAEKREGAER 57
DB 328 LHHYQLQESTVRALFFKEGLFSKEQVAFSTQHPRELSIORVHYLYAYEAK----- 381
QY 58 ILKMNQGRGALFQDLQPSQDEWGTTPDAMKAIVLEKSLNALDLH--ALGSKKA 114
DB 382 -----SAFHIDTQNPILKAMEYTLATLAD-----SQTISNHLRLALGWSK 424
QY 115 DPHLCDFLESHPLDEEVKLIK 135
DB 425 DPHSLVSLVTHFVEEEVENIR 445

RESULT 14
US-09-438-185A-793
Sequence 793, Application US/09438185A
Patent No. 6822071
GENERAL INFORMATION:
APPLICANT: Stephens, Richard
APPLICANT: Mitchell, Wayne
APPLICANT: Kalman, Sue
APPLICANT: Davis, Ronald
TITLE OF INVENTION: The Genome of the University of California
FILE REFERENCE: 018941-000411US
CURRENT APPLICATION NUMBER: US/09/438,185A
CURRENT FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: US 60/108,279
PRIOR FILING DATE: 1998-11-12
PRIOR APPLICATION NUMBER: US 60/128,606
PRIOR FILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 1074
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 793
LENGTH: 998
TYPE: PRT
ORGANISM: Chlamydia pneumoniae
FEATURE:
OTHER INFORMATION: Cpn0791
US-09-438-185A-793

Query Match 9.5%; Score 82; DB 4; Length 998;
Best Local Similarity 24.1%; Pred. No. 7.9;

	Matches	34; Conservative	17; Mismatches	50; Indels	40; Gaps	5
Qy	12	LVLNLYLRASYYLSLGF---	YFRDDVA-----	--LBGVCFFPFLAEKKGBAER		57
	:	:	:	:	:	
Dd	328	LLHHYQLDSESTVRAIFFKEGSLFESKQVAFSTQPRELSEIQRVVYHLYHAEEAK----				381
Qy	58	LLKMVNQNGRALLPDLDQPSODEKGTFPPDAKKAIVLEKSINQALDLH---	-ALGSKKA			114
	:	:	:	:	:	
Dd	382	-----SAPFIHDTONPFLIKAMEYTLATLADA-----	SOPTISNHIRIALGWKSE			424
Qy	115	DPHLCDPLSHPLDEEVKLK	135			
	:	:	:	:	:	
Dd	425	DPHGLSVLTTHFVEEVENIR	445			

RESULT 15

```

US-09-300-909-19
Sequence 19, Application US/09300909
Patent No. 6306580
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: PREPARATION OF HUMAN PAPILLOMAVIRUS B1 HAVING
TITLE OF INVENTION: HELICASE ACTIVITY AND METHOD THEREFOR
NUMBER OF SEQUENCES: 27
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (BFO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/300,909
FLING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/083,942
FLING DATE: 01-MAY-1998
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 629 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-300-909-19

```

Query Match	9.48; Score 80.5; DB 3; Length 629;
-------------	-------------------------------------

Best Local Similarity 21.6%; Pred.No. 6.1;
Matches 22; Conservative 20; Mismatches 37; Indels 23; Gaps 2;

Qy 80 DEWGTPDANKAATLEKSLNQALLDLHALGS-----KKADPHLC 119
| : | : : | : | :
Db 311 DVYGETPEWTERQTVLQHSEFNDTTFPLLSQMWQVAYNDVMDDEIAVKYAQLADSNNAC 370

```
QY      120 DFLESHFLDEEVKLIKMGDHLTNIRLVSKAGIGELYLFE 161
       ||| : : | : : : : : : : : :
Db      371 AFLKS--NSQAKIVKDGTMCRRHYKRAEKRQMSMGWIKSR 409
```

Search completed: August 22, 2005, 09:07:09
Job time : 44 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 22, 2005, 09:06:18 ; Search time 1065 Seconds
(without alignments)
61.404 Million cell updates/sec

Title: US-10-617-955-2-COPY

Perfect score: 860
Sequence: 1 YSTEVEAANVLNVLNLRAS.....VKSAGIGYLFERLTKHD 167

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1759131 seqs, 391586102 residues

Total number of hits satisfying chosen parameters: 1759131

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US10A_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11A_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	850	98.8	167	US-10-617-955-4	Sequence 4, Appl1
2	849	98.7	167	US-10-617-955-2	Sequence 2, Appl1
3	839	97.6	175	US-10-042-865-174	Sequence 174, App
4	799	92.9	167	US-10-142-838B-2	Sequence 2, Appl
5	756	87.9	175	US-09-919-039-333	Sequence 333, App
6	756	87.9	175	US-10-435-666-4	Sequence 4, Appl1
7	756	87.9	175	US-10-262-445-56	Sequence 56, Appl1
8	756	87.9	175	US-10-734-564-128	Sequence 128, Appl
9	756	87.9	175	US-10-684-742-14	Sequence 14, Appl
10	756	87.9	175	US-10-489-740-144	Sequence 144, App
11	756	87.9	254	US-10-104-047-3198	Sequence 3198, App

12	738	85.8	175	US-10-042-865-171	Sequence 171, App
13	738	85.8	175	US-10-732-923-5089	Sequence 5089, App
14	731	85.0	175	US-10-042-865-172	Sequence 172, App
15	730	84.9	183	US-10-042-865-173	Sequence 173, App
16	728	84.7	199	US-10-363-829-400	Sequence 400, App
17	726	84.4	183	US-10-384-496-14	Sequence 14, Appl
18	721	83.8	183	US-10-384-496-10	Sequence 10, Appl
19	721	83.8	183	US-10-042-865-175	Sequence 175, App
20	712	82.8	183	US-10-384-496-8	Sequence 8, Appl1
21	709	82.4	191	US-10-684-742-2	Sequence 2, Appl1
22	673	78.3	160	US-10-732-923-5087	Sequence 5087, App
23	654	76.0	154	US-10-029-386-29603	Sequence 29603, A
24	548	63.7	148	US-09-864-761-19398	Sequence 39398, A
25	493	57.3	181	US-10-617-316-174	Sequence 174, App
26	492	57.2	180	US-10-324-153-4	Sequence 4, Appl1
27	492	57.2	182	US-10-384-496-12	Sequence 12, Appl
28	490	57.0	182	US-10-384-496-6	Sequence 6, Appl1
29	490	57.0	182	US-10-220-335-238	Sequence 238, App
30	487	56.6	183	US-10-384-496-2	Sequence 2, Appl1
31	487	56.6	183	US-10-734-049A-231	Sequence 231, App
32	483	56.2	190	US-10-435-666-8	Sequence 8, Appl1
33	481	55.9	160	US-10-734-564-127	Sequence 127, App
34	481	55.9	164	US-10-732-923-5088	Sequence 5088, App
35	472.5	54.9	184	US-10-425-115-197075	Sequence 197075, A
36	469	54.5	173	US-10-216-464-29	Sequence 29, Appl
37	469	54.5	242	US-10-324-153-2	Sequence 2, Appl
38	468.5	54.5	175	US-10-732-923-5079	Sequence 5079, App
39	439.5	51.1	171	US-10-732-923-5077	Sequence 5077, App
40	436	50.7	99	US-10-425-115-189990	Sequence 189990, App
41	434	50.5	181	US-10-732-923-5086	Sequence 5086, App
42	431	50.1	149	US-10-732-923-5085	Sequence 5085, App
43	425	49.4	101	US-10-425-115-207417	Sequence 207417, A
44	420	48.8	183	US-09-801-544-70	Sequence 70, Appl
45	419.5	48.8	172	US-10-732-923-4972	Sequence 4972, App

ALIGNMENTS

RESULT 1
US-10-617-955-4 Application US10617955

Publication No. US20040142164A1

GENERAL INFORMATION: Matsushita Electric Industrial Co., Ltd.

APPLICANT: Yamashta, Ichiro

TITLE OF INVENTION: FINE PARTICLE FILM AND PRODUCING METHOD OF THE SAME

FILE REFERENCE: 061352-0039

CURRENT APPLICATION NUMBER: US/10/617,955

CURRENT FILING DATE: 2003-07-16

PRIOR APPLICATION NUMBER: PCT/JP02/11954

PRIOR FILING DATE: 2002-11-07

PRIOR APPLICATION NUMBER: 2001-343526

PRIOR FILING DATE: 2001-11-08

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIn version 3.2

SEQ ID NO 4

LENGTH: 167

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Recombinant Liver of Apoferritin of Equus caballus

US-10-617-955-4

Query Match 98.8%, Score 850, DB 16, Length 167;

Best Local Similarity 98.8%, Pred. No. 2.9e-81;

Matches 165; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSTEVEAANVLNVLNLRAS...VKSAGIGYLFERLTKHD 60

DB 1 YSTEVEAANVLNVLNLRAS...VKSAGIGYLFERLTKHD 60

QY 61 MONGRGALPQDQKPSQDWMGTTTDDMKAAIVLEKSLNQLDLHAGSKADPHLCD 120

APPLICANT: Gerlach, Valerie L
 APPLICANT: Edinger, Shlomik R
 APPLICANT: Rothenberg, Mark E
 APPLICANT: Ellerman, Karen
 APPLICANT: MacDougall, John
 APPLICANT: Malyankar, Uriel M
 APPLICANT: Millet, Isabelle
 APPLICANT: Peyman, John
 APPLICANT: Smithson, Glenda
 APPLICANT: Gunther, Erik
 APPLICANT: David
 TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
 TITLE OF INVENTION: Using the Same
 FILE REFERENCE: 21402-537
 CURRENT APPLICATION NUMBER: 05/10/042,865
 PRIOR FILING DATE: 2002-05-17
 PRIOR APPLICATION NUMBER: 60/260,417
 PRIOR FILING DATE: 2001-01-09
 PRIOR APPLICATION NUMBER: 60/260,831
 PRIOR FILING DATE: 2001-01-10
 PRIOR APPLICATION NUMBER: 60/272,338
 PRIOR FILING DATE: 2001-02-28
 PRIOR APPLICATION NUMBER: 60/274,876
 PRIOR FILING DATE: 2001-03-09
 PRIOR APPLICATION NUMBER: 60/284,704
 PRIOR FILING DATE: 2001-04-18
 NUMBER OF SEQ ID NOS: 264
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 174
 LENGTH: 175
 TYPE: PRT
 ORGANISM: Equus caballus
 US-10-042-865-174

Query Match 97.6%; Score 839; DB 15; Length 175;
 Best Local Similarity 97.6%; Pred. No. 4,4e-80;
 Matches 163; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YSTEVEAAVNRVLVNLIRASTYTLISLGFPYDRDDVALEGVCHFFREIAEKRREGAERLLK 60
 Db 9 YSTEVEAAVNRVLVNLIRASTYTLISLGFPYDRDDVALEGVCHFFREIAEKRREGAERLLK 68
 Qy 61 MGNRGRALFODIQKSDSEMGTPDAMKRAATVLEKSNQALDLDAAGSKKADPHLK 120
 Db 69 MGNRGRALFODIQKSDSEMGTPDAMKRAATVLEKSNQALDLDAAGSKKADPHLK 128
 Qy 121 FLESHFIDEVYKLKKMGDHLTNIQRLVSKAGIGYLFRLTLKHD 167
 Db 129 FLESHFIDEVYKLKKMGDHLTNIQRLVSKAGIGYLFRLTLKHD 175

RESULT 4
 US-10-142-838B-2
 Sequence 2, Application US/10142838B
 Publication No. US20030124741A1
 GENERAL INFORMATION:
 APPLICANT: Matsushita Electric Industrial Co., Ltd.
 TITLE OF INVENTION: Recombinant cage-like protein, Method for producing the same,
 TITLE OF INVENTION: Precious metal-recombinant cage-like protein complex, Method for
 TITLE OF INVENTION: producing the same and recombinant DNA
 FILE REFERENCE: APOfeifilin DNA PRT
 CURRENT APPLICATION NUMBER: US/10/142,838B
 PRIOR FILING DATE: 2002-12-09
 PRIOR APPLICATION NUMBER: JP-P2001-142983
 PRIOR FILING DATE: 2001-05-14
 NUMBER OF SEQ ID NOS: 2
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 2
 LENGTH: 167
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE: Description of Artificial Sequence: Recombinant Liver Apoferritin
 OTHER INFORMATION:

prov. Filed 4/18/01
 per patent attorney

OTHER INFORMATION: of Equus caballus

FEATURE: NAME/KEY: MUTAGEN
 LOCATION: (46)
 FEATURE: NAME/KEY: MUTAGEN
 LOCATION: (50)
 FEATURE: NAME/KEY: MUTAGEN
 LOCATION: (53)
 FEATURE: NAME/KEY: MUTAGEN
 LOCATION: (56)
 FEATURE: NAME/KEY: MUTAGEN
 LOCATION: (57)
 FEATURE: NAME/KEY: MUTAGEN
 LOCATION: (120)
 FEATURE: NAME/KEY: MUTAGEN
 LOCATION: (123)
 US-10-142-838B-2

Query Match 92.9%; Score 799; DB 14; Length 167;
 Best Local Similarity 93.4%; Pred. No. 6.8e-76;
 Matches 156; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 YSTEVEAANRLVNLVLRASYYTSLGFFPDRDVALGCVHFFRELAEEKREKGAERLLK 60
 DB 1 YSTEVEAANRLVNLVLRASYYTSLGFFPDRDVALGCVHFFRELAEEKREKGAERLLK 60

QY 61 MONORGRALFODLQKPSQDEWGTTPDANKAIVLEKSLNQALLDLHALGSKKADPHLCD 120
 DB 61 MONORGRALFODLQKPSQDEWGTTPDANKAIVLEKSLNQALLDLHALGSKKADPHLCD 120

QY 121 FLESHFLDEEVKLIKMGDHLTNLQRLVSKAGLGEYLFEERLTLLKHD 167
 DB 121 FLESHFLDEEVKLIKMGDHLTNLQRLVSKAGLGEYLFEERLTLLKHD 167

RESULT 5
 US-09-919-039-333
 Sequence 333, Application US/09919039
 Publication No. US20030108871A1
 GENERAL INFORMATION:
 APPLICANT: Kaser, Matthew R.
 TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LAYER CELL CULTURES
 FILE REFERENCE: PA-0035 US
 CURRENT APPLICATION NUMBER: US/09/919,039
 CURRENT FILING DATE: 2002-09-09
 PRIOR APPLICATION NUMBER: 60/722,113
 PRIOR FILING DATE: 2000-07-28
 NUMBER OF SEQ ID NOS: 401
 SOFTWARE: PERL Program
 SEQ ID NO 333
 LENGTH: 175
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc feature
 OTHER INFORMATION: Incyte ID No. US20030108871A1 4005778CD1
 US-09-919-039-333

Query Match 87.9%; Score 756; DB 10; Length 175;
 Best Local Similarity 86.2%; Pred. No. 2.5e-71;
 Matches 144; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 YSTEVEAANRLVNLVLRASYYTSLGFFPDRDVALGCVHFFRELAEEKREKGAERLLK 60
 DB 9 YSTEVEAANRLVNLVLRASYYTSLGFFPDRDVALGCVHFFRELAEEKREKGAERLLK 68

QY 61 MONORGRALFODLQKPSQDEWGTTPDANKAIVLEKSLNQALLDLHALGSKKADPHLCD 120

DB 69 MONORGRALFODLQKPSQDEWGTTPDANKAIVLEKSLNQALLDLHALGSKKADPHLCD 128

QY 121 FLESHFLDEEVKLIKMGDHLTNLQRLVSKAGLGEYLFEERLTLLKHD 167
 DB 129 FLESHFLDEEVKLIKMGDHLTNLQRLVSKAGLGEYLFEERLTLLKHD 175

RESULT 6
 US-10-435-666-4
 Sequence 4, Application US/10435666
 Publication No. US2004006001A1
 GENERAL INFORMATION:
 APPLICANT: CARTER, Daniel C.
 TITLE OF INVENTION: REARRITIN FUSION PROTEINS FOR USE IN VACCINES AND OTHER APPLICATIONS
 FILE REFERENCE: P07624W00/BAS
 CURRENT APPLICATION NUMBER: US/10/435,666
 CURRENT FILING DATE: 2003-05-12
 PRIOR APPLICATION NUMBER: 60/379,145
 PRIOR FILING DATE: 2002-05-10
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 4
 LENGTH: 175
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-435-666-4

Query Match 87.9%; Score 756; DB 15; Length 175;
 Best Local Similarity 86.2%; Pred. No. 2.5e-71;
 Matches 144; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 YSTEVEAANRLVNLVLRASYYTSLGFFPDRDVALGCVHFFRELAEEKREKGAERLLK 60
 DB 9 YSTEVEAANRLVNLVLRASYYTSLGFFPDRDVALGCVHFFRELAEEKREKGAERLLK 68

QY 61 MONORGRALFODLQKPSQDEWGTTPDANKAIVLEKSLNQALLDLHALGSKKADPHLCD 120
 DB 69 MONORGRALFODLQKPSQDEWGTTPDANKAIVLEKSLNQALLDLHALGSKKADPHLCD 128

QY 121 FLESHFLDEEVKLIKMGDHLTNLQRLVSKAGLGEYLFEERLTLLKHD 167
 DB 129 FLESHFLDEEVKLIKMGDHLTNLQRLVSKAGLGEYLFEERLTLLKHD 175

RESULT 7
 US-10-262-445-56
 Sequence 56, Application US/10262445
 Publication No. US20040014058A1
 GENERAL INFORMATION:
 APPLICANT: Alsobrook II, John
 APPLICANT: Burgess, Catherine
 APPLICANT: Catterton, Elina
 APPLICANT: Chant, John
 APPLICANT: Chaudhuri, Amitabha
 APPLICANT: Edinger, Shlomit
 APPLICANT: Gerlach, Valerie
 APPLICANT: Giot, Loic
 APPLICANT: Gorman, Linda
 APPLICANT: Guo, Xiaojia
 APPLICANT: Kekuda, Ramesh
 APPLICANT: Mezes, Peter
 APPLICANT: Millet, Isabelle
 APPLICANT: Ooi, Chean Eng
 APPLICANT: Patirajan, Meera
 APPLICANT: Rieger, Daniel
 APPLICANT: Spytek, Kimberly
 APPLICANT: Taupier Jr., Raymond J.
 APPLICANT: Zernusen, Bryan
 APPLICANT: Zhong, Haihong
 APPLICANT: Zhong, Mei
 TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS O
 TITLE OF INVENTION: THE SAME

```

Db      9      YSTDEAVANSLVNLXYLQASTYTLISGYPFDRDVALGVSHFFPRLAEKKEGVERLLK   68
Oy      61     MONORGGRALFDOLKPSODEWGTTPDAMKAAYIEKSINQALLDLHALGSKADPHLCD   120
          |||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db      69     MONORGGRALFDODIKPAEDWEGKTPDMKAMALEKLNQALLDLHALGSAARTDPHLCD   128
          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Oy      121    FLESHPLDEEYVKLIKMGDHLTNIOFLVKSXNAGLEYLFERLTLLKHD   167
          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
          129 FLETHPLDEEYVKLIKMGDHLTNILRLOGPEAGLEGIFYFERLTLLKHD   175
          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 9
US-10-684-742-14
Sequence 14, Application US/10684742
Publication No. US20040259107A1
GENERAL INFORMATION:
APPLICANT: Bernardino Ghetti
TITLE OF INVENTION: PERRITIN LIGHT SUBUNIT VARIANT-ENCODING
TITLE OF INVENTION: NUCLEIC ACIDS, POLYPEPTIDES, TRANSGENIC ANIMALS COMPRISING
TITLE OF INVENTION: THE SAME, ANTIBODIES THERETO, AND METHODS OF USE THEREOF
FILE REFERENCE: APTI 0253
CURRENT APPLICATION NUMBER: US/10/664,742
CURRENT FILING DATE: 2003-10-14
PRIOR APPLICATION NUMBER: 60/418,126
PRIOR FILING DATE: 2003-10-11
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 14
LENGTH: 175
TYPE: PRT

```

```

US-10-684-742-14

Query Match          87.9%; Score 756; DB 16; Length 175;
Best Local Similarity 86.2%; Pred. No. 2.5e-71;
Matches 144; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

Cy      1  YSTEVEAAVNRLVNLVLTASATYTLSLGFPYPRDDVALBGVCHFPRELAEEKREGAERLLK 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      9  YSTDVEAAVNRLVNLVLTASATYTLSLGFPYPRDDVALBGVSHFPRELAEEKREGYERLLK 68

Cy      61  MONORGGGALFQDLOKPSODEWGTTTDDMKAAIVLEKSLNQALLDLHALGSKKADPHLCD 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      69  MONORGGGALFQDIKKPAADEWEGKTPDDAMKAMALEKLNQALLDLHALGSKARTDPHLCD 128

Cy      121  FLESHPELDEEVKLTIKKMGDHLTNTORLAKSKAGLEYLPERLTLRKD 167
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      129  FLETHPELDEEVKLTIKKMGDHLTNTLRGLGPEKAGLEYLPERLTLRKD 175

RESULT 10
US-10-489-740-14
; Sequence 144, Application US/10489740
; Publication No. US20050112574A1
; GENERAL INFORMATION:
; APPLICANT: Biomedics Limited
; TITLE OF INVENTION: P9
; FILE REFERENCE: Angiogenesis PCT
; CURRENT APPLICATION NUMBER: US/10/489,740
; CURRENT FILING DATE: 2004-03-15
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 144
; LENGTH: 175
; TYPE: PRT

```

US-10-489-740-144

Query Match	87.9%	Score 756;	DB 17;	Length 175;
Best Local Similarity	86.2%;	Pred. No. 2.5e+11;		
Matches 144; Conservative	11;	Mismatches 12;	Indels 0;	Gaps 0;

```

QY 1 YSTEVEAAVNRLVNLVLRASYTSLGFFPRDDVALGCVHFFRELAEEKREGAERLLK 60
DB 9 YSTVEAAVNSLVNLVYQASYYTSLGFFPRDDVALGCVHFFRELAEEKREGAERLLK 68
QY 61 MONORGRALFODLOKPSQDEWGTTPDAMKAAIVLEKSLNQALLDLHALGSKKADPHLCD 120
DB 69 MONORGRALFODLOKPSQDEWGTTPDAMKAAIVLEKSLNQALLDLHALGSKKADPHLCD 128
QY 121 FLESHFLDEEYVLIKKMGDHLTNLQRLVSKAGLGEYLFERLTLKHD 167
DB 129 FLESHFLDEEYVLIKKMGDHLTNLRLGSPAGLGEYLFERLTLKHD 175

RESULT 11
US-10-104-047-3198
; Sequence 3198, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3198
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-3198

```

```

Query Match 87.9%; Score 756; DB 15; Length 254;
Best Local Similarity 86.2%; Pred. No. 4e-71;
Matches 144; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 YSTEVEAAVNRLVNLVLRASYTSLGFFPRDDVALGCVHFFRELAEEKREGAERLLK 60
DB 8 YSTVEAAVNSLVNLVYQASYYTSLGFFPRDDVALGCVHFFRELAEEKREGAERLLK 147
QY 61 MONORGRALFODLOKPSQDEWGTTPDAMKAAIVLEKSLNQALLDLHALGSKKADPHLCD 120
DB 148 MONORGRALFODLOKPSQDEWGTTPDAMKAAIVLEKSLNQALLDLHALGSKKADPHLCD 207
QY 121 FLESHFLDEEYVLIKKMGDHLTNLQRLVSKAGLGEYLFERLTLKHD 167
DB 129 FLESHFLDEEYVLIKKMGDHLTNLRLGSPAGLGEYLFERLTLKHD 254

```

```

RESULT 12
US-10-042-865-171
; Sequence 171, Application US/10042865
; Publication No. US20040029216A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Li, Li
; APPLICANT: Zernusen, Bryan D
; APPLICANT: Casman, Stacie J
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zhong, Mei
; APPLICANT: Gangoli, Bsha A
; APPLICANT: Burgess, Catherine E
; APPLICANT: Paturajan, Meera
; APPLICANT: Verneet, Corine A.M
; APPLICANT: Taylor, Sarah
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Miller, Charles E
; APPLICANT: Guo, Xiaojia
; APPLICANT: Boldog, Ference L
; APPLICANT: Grose, William M
; APPLICANT: Alsbrook II, John P

```

```

; APPLICANT: Gerlach, Valerie L
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Malyankar, Uziel M
; APPLICANT: Miller, Isabelle
; APPLICANT: Peyman, John
; APPLICANT: Smithson, Glenda
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, David
; TITLE OF INVENTION: Using the Same
; FILE REFERENCE: 21402-537
; CURRENT APPLICATION NUMBER: US/10/042,865
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/260,417
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/260,831
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 60/272,338
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/274,876
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/284,704
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 264
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 171
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-042-865-171

```

```

Query Match 85.8%; Score 738; DB 15; Length 175;
Best Local Similarity 83.8%; Pred. No. 1.9e-69;
Matches 140; Conservative 15; Mismatches 12; Indels 0; Gaps 0;

QY 1 YSTEVEAAVNRLVNLVLRASYTSLGFFPRDDVALGCVHFFRELAEEKREGAERLLK 60
DB 9 YSTEVEAAVNRLVNLVLRASYTSLGFFPRDDVALGCVHFFRELAEEKREGAERLLK 68
QY 61 MONORGRALFODLOKPSQDEWGTTPDAMKAAIVLEKSLNQALLDLHALGSKKADPHLCD 120
DB 69 LONORGRALFLDVQKPSQDEWGTTPDAMKAAIVLEKSLNQALLDLHALGSKKADPHLCD 128
QY 121 FLESHFLDEEYVLIKKMGDHLTNLQRLVSKAGLGEYLFERLTLKHD 167
DB 129 FLESHFLDEEYVLIKKMGDHLTNLRLGSPAGLGEYLFERLTLKHD 175

```

```

RESULT 13
US-10-732-923-5089
; Sequence 5089, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 5089
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-10-732-923-5089

```

```

Query Match 85.8%; Score 738; DB 17; Length 175;
Best Local Similarity 85.6%; Pred. No. 1.9e-69;
Matches 143; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

```

	Matches	141; Conservative	14; Mismatches	12; Indels	0; Gaps	0;
QY	1	YSTEVEAAVNFLVNLVLYLPASTTYISLGFYPRDRDVALRGVGHFRELAEKREGAEKRLIK				60
Db	9	YSTEVEAAVNFLVNLVNLH:QASTYTYISLGFYPRDRDVALAAGVGHFRELAKEREKAEKRLIK				68
QY	61	MONRGGRALFQDQKPSQODEWGTTPDDAKAIYLEKSLNQALLDHLHLSGSKKADPHLCD				120
Db	69	TQNRGGRALFQDVQKPSQODEWGTTPDDAKAIYLEKSLNQALLDHLHLSGSAKTDSSHCD				128
QY	121	FLSHGFLDEEVYKLIKMGDHLTNITQRLVKSAGSIGEYIFERLTLKHD				167

```

RESULT 15
US-10-042-865-173
; Sequence 173, Application US/10042865
; Publication No. US20040029216A1
; GENERAL INFORMATION:
APPLICANT: Padigaru, Muralidhara
APPLICANT: Li, Li
APPLICANT: Zernhusen, Bryan D
APPLICANT: Caeman, Stacie J
APPLICANT: Shenoy, Suresh G
APPLICANT: Spytek, Kimberly
APPLICANT: Zhong, Mei
APPLICANT: Gangolli, Esha A
APPLICANT: Burgess, Catherine E
APPLICANT: Paturajan, Meera
APPLICANT: Vernet, Corine A.M
APPLICANT: Taylor, Sarah
APPLICANT: Tchernev, Velizar T
APPLICANT: Miller, Charles B
APPLICANT: Guo, Xiaojia
APPLICANT: Boldog, Ferenc L
APPLICANT: Grose, William M
APPLICANT: Alsbrook II, John P
APPLICANT: Gerlach, Valerie L
APPLICANT: Edinger, Shlomit R
APPLICANT: Rothenberg, Mark E
APPLICANT: Ellerman, Karen
APPLICANT: MacDougall, John
APPLICANT: Malyankar, Uriel M
APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John
APPLICANT: Smithson, Glenda
APPLICANT: Gunther, Erik
APPLICANT: Stone, David
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-537
CURRENT APPLICATION NUMBER: US/10/042,865
CURRENT FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/260,417
PRIOR FILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: 60/260,831
PRIOR FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: 60/272,338
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/274,876
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/284,704
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 264
SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 173
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-042-865-173

```

Best Local Similarity 81.7%; Pred. No. 1.4e-68;
Matches 143; Conservative 15; Mismatches 9; Indels 8; Gaps 1;

Qy	1	YSTEVEAAVNRLVNLVYLRLASYTYLSLGFYFDRDDVALEGVCHFFRELAEEKREGAERLLK	60
		: : : : : : : : :	
Db	9	YSTEVEAAVNRLVNLVNLHRLASYYLSLGFYFDRDDVALEGVCHFFRELAEEKREGAERLLK	68
		: : : : : : : :	
Qy	61	MONORGGPALFQDLQKPSQDEWGTTPDAMKAALIVLEKSLNQLDHALGSKADPHLCD	120
		: : : : : : : : :	
Db	69	LQNERGGPALFQDYQKPSQDEWGKTLFAMKAALALEKNINQALDLHALGSAQADPHLCD	128
		: : : : : : : : :	
Qy	121	FLSHFLDEEYKLIKMGDHLTNLOR-----LVKSKAGLGEYLFERLTLTKHD	167
		: : : : : : : :	
Db	129	FLSHFLDKKEVKLIKMGVHLLTNLRKQGPQAPQTGVAQASLGEYLFERLTLTKHD	183
		: : : : : : : :	

Search completed: August 22, 2005, 09:28:43
Job time : 1066 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 22, 2005, 09:06:18 ; Search time 165 Seconds
(without alignments)
391.448 Million cell updates/sec

Title: us-10-617-955-2-COPY

Perfect score: 860
Sequence: 1 YSTEVEAAVNRLLNLYLRAS.....VKSRAGLGEYLPRLTLKHD 167

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003s:*
7: geneseqp2003ds:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	850	98.8	167	6	ABR56248
2	849	98.7	167	6	ABR56247
3	799	92.9	167	6	ABP57965
4	756	87.9	175	6	ABR64209
5	756	87.9	175	6	ABU89807
6	756	87.9	175	7	ADG42356
7	756	87.9	175	8	ADG71168
8	756	87.9	175	8	ADN11575
9	756	87.9	175	8	ADQ26090
10	756	87.9	175	8	ADQ29702
11	756	87.9	175	8	ABM62153
12	756	87.9	254	7	ADB55044
13	756	87.9	362	8	ADQ82746
14	753	87.6	238	4	AAU29923
15	742	86.3	175	8	ADQ60419
16	741.5	86.2	261	4	AAU29988
17	729.5	84.8	177	4	AAU31122
18	728	84.7	199	5	ABP51378
19	726	84.4	175	8	ADQ09362
20	709	82.4	191	8	ADN11563
21	658	76.5	131	4	ABG15651
22	654	76.0	154	8	ABO55969
23	548	63.7	148	4	AAU19617
24	548	63.7	148	4	ABB39270
25	548	63.7	148	4	AAU32772

26	548	63.7	148	4	ABB24100	Abb24100 Protein #
27	548	63.7	148	4	AAU72528	Aau72528 Human bon
28	548	63.7	148	4	AAU59934	Aau59934 Human bra
29	548	63.7	148	4	ABG54219	Abg54219 Human liv
30	548	63.7	148	5	ABG42348	Abg42348 Human pep
31	530	61.6	114	6	ABU70554	Abu70554 Human adi
32	490	57.0	180	5	ABP69305	Abp69305 Human pol
33	490	57.0	182	4	AAU27741	Aau27741 Mouse ful
34	490	57.0	227	6	ABU11456	Abu11456 Human MDD
35	487	56.6	183	2	AAU71567	Aau71567 Human mon
36	487	56.6	183	4	AAU90804	Aau90804 Human bne
37	487	56.6	183	7	ADD22444	Add22444 HLA-B46 T
38	487	56.6	183	7	ADL15887	Adl15887 Human pp
39	487	56.6	183	8	ABM81295	Abm81295 Tumour-as
40	487	56.6	206	5	ABR97273	AbR97273 Novel hum
41	487	56.5	183	7	ADN31067	Adn31067 Human H-C
42	483	56.2	190	7	ADG42360	Adg42360 Ferritin
43	483	56.2	190	8	ADQ29701	AdQ29701 Human col
44	483	56.2	190	8	ADP24691	AdP24691 PRO polyP
45	469	54.5	173	4	AAE09630	Aae09630 Human gen

ALIGNMENTS

RESULT 1	ABR56248	standard; protein; 167 AA.
ID	ABR56248	
XX	ABR56248	
AC	ABR56248	
XX	20-NOV-2003	(first entry)
DT	XX	
XX	XX	Horse liver apoferritin #2.
DE	XX	
XX	XX	Horse; liver apoferritin.
KW	XX	
XX	XX	Equus caballus.
OS	XX	
XX	XX	
PH	XX	Location/Qualifiers
FT	XX	Misc-difference 112..113
FT	XX	/note= "Encoded by AGG AGG"
FT	XX	Misc-difference 149
FT	XX	/note= "Encoded by GGC"
FT	XX	Misc-difference 151
FT	XX	/note= "Encoded by CAA"
XX	XX	
PN	XX	MO2003040025-A1.
XX	XX	
PD	XX	15-MAY-2003.
XX	XX	
PF	XX	07-NOV-2002; 2002WO-JP011594.
XX	XX	
PR	XX	08-NOV-2001; 2001JP-00343526.
XX	XX	
PA	XX	(MATU) MATSUSHITA ELECTRIC IND CO LTD.
XX	XX	Yamashita I; INVENTOR
PI	XX	
XX	XX	MP1: 2003-468508/44.
DR	XX	N-PSDB; ACC70678.
XX	XX	
PT	XX	Film used in analysis of protein crystal structure by electron
XX	XX	microscopy, and in manufacturing float gates and magnetic disks contains
PT	XX	micrograins of proteins aligned regularly at high density.
XX	XX	
PS	XX	Disclosure; Page 43-44; 47pp; Japanese.
XX	XX	
CC	XX	The present invention relates to a micrograin film, comprising a
XX	XX	substrate and micrograins made of proteins that are regularly arranged on
CC	XX	the surface of the substrate in the plane direction parallel to the
CC	XX	surface. The film is useful in analysis of protein crystal structure by
CC	XX	electron microscopy, and in manufacturing float gates of EP-ROM or E2P-

Matches 156; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 YSTEVEAAVNRLVNLVLRASYTYLSLGFYFDRDVALGVCFFPRLAEKREGAERLLK 60
DB 1 YSTEVEAAVNRLVNLVLRASYTYLSLGFYFDRDVALGVCFFPRLAEKREGAERLLK 60

QY 61 MONORGGRALFQDLQKPSODEWGTTPDAMKAAIVLEKSLNQALLDLHALGSKKADPHLCD 120
DB 61 MONORGGRALFQDLQKPSODEWGTTPDAMKAAIVLEKSLNQALLDLHALGSKKADPHLCD 120

QY 121 FLESHFLDEEVYKLIKMGDHLTNLQRLVYKSAAGLGEYLFERLTLKHD 167
DB 121 FLESHFLDEEVYKLIKMGDHLTNLQRLVYKSAAGLGEYLFERLTLKHD 167

RESULT 4
ABR64209
ID ABR64209 standard; protein; 175 AA.
AC ABR64209;
XX
XX 15-OCT-2003 (first entry)
XX
DE Angiogenesis protein BNO103.
XX
XX Cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
XX antiapoptotic; antiarteriosclerotic; cardiac; vasotropic; angiogenesis;
XX gene therapy; vasculature; cancer; rheumatoid arthritis; psoriasis;
XX diabetic retinopathy; cardiovascular disease; atherosclerosis;
XX ischemic limb disease; coronary artery disease.
XX
XX Homo sapiens.
XX
XX WO2003027285-A1.
XX
XX 03-APR-2003.
XX
XX 19-SEP-2002; 2002WO-AU001282.
XX
XX 27-SEP-2001; 2001AU-00007973.
XX 27-SEP-2001; 2001AU-00007974.
XX 11-OCT-2001; 2001AU-00008210.
XX 29-OCT-2001; 2001AU-00008532.
XX 13-NOV-2001; 2001AU-00008838.
XX 28-AUG-2002; 2002AU-00951032.
XX
XX (BION-) BIONOMICS LTD.
XX
XX Gamble JR, Hahn CN, Vadas MA;
XX
XX WPI; 2003-354655/33.
XX N-PSDB; ACP34484.
XX
XX New angiogenic genes and polypeptides, useful for diagnosing,
XX prognosticating or treating an angiogenesis-related disorder, e.g.
XX cancer, rheumatoid arthritis, diabetic retinopathy, psoriasis or
XX cardiovascular diseases.
XX
XX Claim 15; SEQ ID NO 144; 90pp; English.

XX
XX The invention relates to the isolation of novel genes (ACP34446-ACP34559)
XX encoding proteins (ABR64180-ABR64281) involved in the process of
XX angiogenesis. The nucleic acid molecules are useful in identifying and/or
XX obtaining full-length human genes involved in an angiogenic process. The
XX nucleic acid molecule, polypeptides or complexes encoded, cells or
XX genetically modified non-human animals derived from these are useful for
XX the screening of candidate pharmaceutical compounds used in treating
XX angiogenesis-related disorders. They are also useful for diagnosing,
XX prognosticating or treating an angiogenesis-related disorder, which
XX involves uncontrolled or enhanced angiogenesis or is a disorder in which
XX a decreased vasculature is of benefit (e.g. cancer, rheumatoid arthritis,
XX diabetic retinopathy, psoriasis or cardiovascular diseases such as
XX atherosclerosis), or involves inappropriately arrested or decreased

CC angiogenesis or is a disorder in which an expanding vasculature is of
CC benefit (e.g. ischemic limb disease or coronary artery disease). The
CC modulator of expression or activity of the polypeptide encoded by the
CC nucleic acid sequence is useful for manufacturing a medicament for the
CC treatment of an angiogenesis-related disorder. This sequence corresponds
CC to one of the novel angiogenic protein

XX
XX Sequence 175 AA:
SQ
QY 1 YSTEVEAAVNRLVNLVLRASYTYLSLGFYFDRDVALGVCFFPRLAEKREGAERLLK 60
DB 9 YSTEVEAAVNRLVNLVLRASYTYLSLGFYFDRDVALGVCFFPRLAEKREGAERLLK 68

QY 61 MONORGGRALFQDLQKPSODEWGTTPDAMKAAIVLEKSLNQALLDLHALGSKKADPHLCD 120
DB 61 MONORGGRALFQDLQKPSODEWGTTPDAMKAAIVLEKSLNQALLDLHALGSKKADPHLCD 128

QY 121 FLESHFLDEEVYKLIKMGDHLTNLQRLVYKSAAGLGEYLFERLTLKHD 167
DB 129 FLESHFLDEEVYKLIKMGDHLTNLQRLVYKSAAGLGEYLFERLTLKHD 175

RESULT 5
ABU89807
ID ABU89807 standard; protein; 175 AA.
AC ABU89807;
XX
XX 10-JUL-2003 (first entry)
XX
XX Novel human protein NOV18C.
XX
XX Human; cytosolic; DAPK3-Agonist; DAPK3-Antagonist; cancer; NOV.
XX
XX Homo sapiens.
XX
XX WO2003031571-A2.
XX
XX 17-APR-2003.
XX
XX 02-OCT-2002; 2002WO-US031357.
XX
XX 05-OCT-2001; 2001US-0327454P.
XX 09-OCT-2001; 2001US-0327917P.
XX 09-OCT-2001; 2001US-0328029P.
XX 09-OCT-2001; 2001US-0328056P.
XX 12-OCT-2001; 2001US-0328849P.
XX 15-OCT-2001; 2001US-0329414P.
XX 17-OCT-2001; 2001US-0330142P.
XX 22-OCT-2001; 2001US-0341058P.
XX 24-OCT-2001; 2001US-0343629P.
XX 29-OCT-2001; 2001US-0349575P.
XX 01-NOV-2001; 2001US-0346357P.
XX 25-JUN-2002; 2002US-0391342P.
XX 01-OCT-2002; 2002US-00262445.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Alsobrook JP, Burgess CE, Catterton E, Chant JS, Chaudhuri A;
XX Edlinger SR, Gerlach VL, Giot L, Gorman L, Guo X, Kekuda R;
XX Mezes PS, Miller I, Ooi CE, Patuturajan M, Rieger DK, Spytek KA;
XX Taupier RJ, Zernusen BD, Zhong H, Zhong M;
XX WPI; 2003-381704/36.
XX N-PSDB; ACP90184.
XX
XX New DAPK3 polypeptide, useful for preparing a composition for treating or
XX preventing e.g., cancer.

CC protein which involves combining the protein encoded by the cDNA with
 CC several of molecules or compounds under conditions to allow specific
 CC binding, and detecting specific binding between the protein and a
 CC molecule or compound, therefore identifying a ligand which specifically
 CC binds the protein. The composition is useful for detecting and
 CC quantifying differential gene expression, can be used in gene therapy, to
 CC formulate prognosis and to design a treatment regimen and to monitor the
 CC efficacy of treatment. The present sequence represents the amino acid
 CC sequence of a protein encoded by a cDNA differentially expressed in a
 CC liver disorder.

CC Sequence 175 AA;

Query Match 87.9%; Score 756; DB 8; Length 175;
 Best Local Similarity 86.2%; Pred. No. 2.4e-70;
 Matches 144; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 YSTEVEAAVNLVNLVYLRASTYTLGLGFYPRDDVALGVCFFRELAEKREGAERLLK 60
 DB 9 YSTDVEAAVNSLVNLVQLQASTYTLGLGFYPRDDVALGVCFFRELAEKREGAERLLK 68
 QY 61 MONORGRALFQDLQKPSQDEWGTTPDAMKAIVLEKSLNQLDLHLGSKKADPHLCD 120
 DB 69 MONORGRALFQDIKKPADEWGTTPDAMKAAMALEKLNQLDLHLGSKARTDPHLCD 128
 QY 121 FLESHFLDEBYKLKKMGDHLTNLQRLVKSAGLGEYLFERLTLLKHD 167
 DB 129 FLETHFLDEBYKLKKMGDHLTNLRLGSPAGLGEYLFERLTLLKHD 175

RESULT 8
 ADN11575

ID ADN11575 standard; protein; 175 AA.

XX ADN11575;

DT 15-JUL-2004 (first entry)

XX Human wild-type ferritin light chain protein.

XX neuroprotective; neurodegenerative disease; FTL;

KM ferritin light chain variant; iron deposition; human.

XX Homo sapiens.

XX WO2004033661-A2.

XX 22-APR-2004.

XX 14-OCT-2003; 2003WO-US032412.

XX 11-OCT-2002; 2002US-0418126P.

XX (ADRE-) ADVANCED RES & TECHNOLOGY INST.

XX Vidal R, Ghetti B;

XX WPI; 2004-340922/31.

XX N-PSDB; ADN11574.

XX New isolated polynucleotide encoding ferritin light chain variant

XX polypeptide, useful for treating diseases related to aberrant ferritin

XX and/or iron deposition which affect other organ systems, or

XX neurodegenerative diseases.

XX Example 1; Fig 7B; 107pp; English.

XX The present invention provides the protein and coding sequences of a

XX human ferritin light chain variant polypeptide. The nucleic acid encoding

XX ferritin light chain variant polypeptide, the polypeptides and antibodies

XX are useful as research tools to examine the role of ferritin light

XX polypeptide (FTL) in the development of neurodegenerative disease,

XX identify binding partners of FTL variant polypeptides, identify signaling

CC pathways which regulate FTL variant expression, and screen for and
 CC characterize agents capable of modulating FTL variant activity. The
 CC nucleic acids can also be used as probes to detect the presence of and/or
 CC expression of genes encoding FTL variant-like proteins. It can also be
 CC used to create recombinant cell lines for use in assays to identify
 CC agents, which modulate FTL variant mediated regulation of aberrant
 CC ferritin and iron deposition. Agents capable of modulating FTL variant
 CC activity are useful for treating diseases related to aberrant ferritin
 CC and/or iron deposition which affect other organ systems, and
 CC neurodegenerative diseases. The present sequence is the human wild-type
 CC FTL protein.

CC Sequence 175 AA;

Query Match 87.9%; Score 756; DB 8; Length 175;
 Best Local Similarity 86.2%; Pred. No. 2.4e-70;
 Matches 144; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 YSTEVEAAVNLVNLVYLRASTYTLGLGFYPRDDVALGVCFFRELAEKREGAERLLK 60
 DB 9 YSTDVEAAVNSLVNLVQLQASTYTLGLGFYPRDDVALGVCFFRELAEKREGAERLLK 68
 QY 61 MONORGRALFQDLQKPSQDEWGTTPDAMKAIVLEKSLNQLDLHLGSKKADPHLCD 120
 DB 69 MONORGRALFQDIKKPADEWGTTPDAMKAAMALEKLNQLDLHLGSKARTDPHLCD 128
 QY 121 FLESHFLDEBYKLKKMGDHLTNLQRLVKSAGLGEYLFERLTLLKHD 167
 DB 129 FLETHFLDEBYKLKKMGDHLTNLRLGSPAGLGEYLFERLTLLKHD 175

RESULT 9
 ADQ26090

ID ADQ26090 standard; protein; 175 AA.

XX ADQ26090;

DT 23-SEP-2004 (first entry)

XX Light polypeptide ferritin.

XX BDEC; brain capillary endothelial cell; astrocyte; permeability;

XX endothelial cell; pro-barrier; PB;

XX microvascular permeability-modifying disorder;

XX neurodegenerative disorder; cerebrovascular accident;

XX Alzheimer's disease; vascular-related dementia;

XX Creutzfeldt-Jacob disease; bovine spongiform encephalopathy;

XX Parkinson's disease; brain trauma; multiple sclerosis;

XX peripheral disorder; septic shock; hepatic encephalopathy;

XX diabetic hypertension; diabetic microangiopathy; sleeping sickness;

XX neuropsychiatric disorder; depression; autism; schizophrenia; psychosis;

XX CNS disorder; brain tumor; epilepsy; migraine; narcolepsy; insomnia;

XX chronic fatigue syndrome; mountain sickness; AIDS-related dementia;

XX angioneurotic-related disorder; proliferative vitreoretinopathy;

XX rheumatoid arthritis; Crohn's disease; atherosclerosis;

XX ovarian hyperstimulation; psoriasis; endometriosis; neovascularisation;

XX restenosis; balloon angioplasty; scar tissue overproduction;

XX peripheral vascular disease; hypertension; inflammatory vasculitides;

XX Reynaud's disease; Reynaud's phenomenon; aneurysm; arterial restenosis;

XX thrombophlebitis; lymphangitis; lymphedema; wound healing; tissue repair;

XX ischaemia reperfusion injury; angina; myocardial infarction;

XX chronic heart condition; osteoporosis; light polypeptide ferritin; FTL.

XX Homo sapiens.

XX WO2004056386-A2.

XX 08-JUL-2004.

XX 19-DEC-2003; 2003WO-NL000915.

XX 19-DEC-2002; 2002EP-00080503.

XX 25-APR-2003; 2003US-0465234P.

XX (UYLE-) RIJKSUNIV LEIDEN.
 XX
 XX
 XX Galliard PJ, De Boer AG, Brink A,
 XX
 DR WPI; 2004-500264/47.

XX Modulating the permeability of endothelial cells, useful for treating or
 PT preventing e.g. neurodegenerative disorders, comprises altering in the
 PT endothelial cells the activity or the steady-state level of a pro-barrier
 PT polypeptide.

XX Claim 1; SEQ ID NO 44; 222pp; English.

XX This sequence represents light polypeptide ferritin encoded by the FTL
 CC gene. This protein is upregulated in BCEC (brain capillary endothelial
 CC cells) by physical co-culture with astrocytes. This protein sequence may
 CC be used in the method of the invention for modulating the permeability of
 CC endothelial cells. The method comprises altering in the endothelial cells
 CC the activity or the steady-state level of a pro-barrier (PB) polypeptide
 CC having an amino acid sequence having at least 90% identity with a claimed
 CC amino acid sequence selected from ADQ26047ADQ26048ADQ26049ADQ26050ADQ2605
 CC 1ADQ26052ADQ26053ADQ26054ADQ26055ADQ26056ADQ26057ADQ26058ADQ26059ADQ2606
 CC ADQ26061ADQ26062ADQ26063ADQ26064ADQ26065ADQ26066ADQ26067ADQ26068ADQ26069A
 CC DQ26070ADQ26071ADQ26072ADQ26073ADQ26074ADQ26075ADQ26076ADQ26077ADQ26078AD
 CC Q26079ADQ26080ADQ26081ADQ26082ADQ26083ADQ26084ADQ26085ADQ26086ADQ26087AD
 CC 26088ADQ26089ADQ26090ADQ26091ADQ26092ADQ26093ADQ26094ADQ26095ADQ26096ADQ2
 CC 6097ADQ26098ADQ26099. The PB polypeptides, nucleic acid molecules
 CC encoding them, antagonists or a gene therapy vector comprising an
 CC antisense nucleotide sequence capable of inhibiting the expression of the
 CC nucleotide sequence encoding a PB polypeptide, are useful in the
 CC manufacture of a composition for treating or preventing the expression of the
 CC permeability-modifying disorder, including neurodegenerative disorders
 CC (e.g. cerebrovascular accidents, Alzheimer's disease, vascular-related
 CC dementia, Creutzfeldt-Jacob disease, bovine spongiform encephalopathy,
 CC Parkinson's disease, brain trauma, multiple sclerosis), peripheral
 CC disorders with a CNS component (such as septic shock, hepatic
 CC encephalopathy), (diabetic) hypertension, diabetic microangiopathy or
 CC sleeping sickness), neuropsychiatric disorders (e.g. depression, autism,
 CC schizophrenia and other psychoses), other CNS disorders (brain tumours,
 CC epilepsy, migraine, narcolepsy, insomnia, chronic fatigue syndrome,
 CC mountain sickness, or AIDS-related dementia), and angiotensin-related
 CC disorders (proliferative vitreoretinopathy, rheumatoid arthritis, Crohn's
 CC disease, atherosclerosis, ovarian hyperstimulation, psoriasis,
 CC endometriosis associated with neovascularisation, restenosis subsequent
 CC to balloon angioplasty, scar tissue overproduction, peripheral vascular
 CC disease, hypertension, inflammatory vasculitides, Reynaud's disease,
 CC Reynaud's phenomenon, aneurysms, arterial restenosis, thrombophlebitis,
 CC lymphangitis, lymphedema, wound healing and tissue repair, ischemia
 CC reperfusion injury, angina, myocardial infarctions, chronic heart
 CC conditions, or osteoporosis). The PB polypeptide may also be used in the
 CC manufacture of a composition for reversibly increasing the microvascular
 CC permeability in a subject.

XX Sequence 175 AA;

Query Match 87.9%; Score 756; DB 8; Length 175;

Best Local Similarity 86.2%; Pred. No. 2.4e-70;

Matches 144; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 YSTEVEAAVNRVLVNLVLRASVYTLISLGFYPRDDVALGVCFFPRLAEKREKREGARLLK 60
 DB 9 YSTDVEAAVNSLVNLVYLQASVYTLISLGFYPRDDVALGVCFFPRLAEKREKREGARLLK 68
 QY 61 MONORGRALFODLOKPSODEWGTTPDAMKAAVLEKSLNQALLDLHALGSKKADPHL 120
 DB 69 MONORGRALFODIKKPADEWGTTPDAMKAAVLEKSLNQALLDLHALGSKKADPHL 128
 QY 121 FLESHFLDEEVKLIKKGMDHLTNLQRLVYSKAGLGEVLFERLLTKHD 167
 DB 129 FLESHFLDEEVKLIKKGMDHLTNLQRLVYSKAGLGEVLFERLLTKHD 175

RESULT 10
 ADQ29702
 ID ADQ29702 standard; protein; 175 AA.

XX
 AC ADQ29702;

DT 07-OCT-2004 (first entry)

DE Human colorectal cancer-associated protein #57.

KM human; colon cancer; TIMP1; Reg1-alpha;

KM colorectal cancer-associated marker.

XX Homo sapiens.

XX EPI439393-A2.

XX 21-JUL-2004.

XX 15-DEC-2003; 2003EP-00257868.

XX 13-DEC-2002; 2002US-0433554P.

XX 31-JUL-2003; 2003US-0491387P.

XX (PARB) BAYER HEALTHCARE LLC.

XX (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.

PI Asile JH, Boardman LA, Bugart LJ, Burgess CC, Catino TJ;

PI Dwtivedi P, Huntress M, Johnson KA, Lewis ME, Malmonis PJ, Myerow SH;

PI Brown-Shimer SLA, Thagalingam A, Thibodeau SN, Molino GA;

XX WPI; 2004-545561/53.

DR N-PSDB; ADQ29635.

PT Diagnosing colon cancer in individual, preferably human, by detecting

PT presence of TIMP 1 in sample, where presence of TIMP 1 in sample is

PT indicative of colon cancer in individual.

XX Claim 7; SEQ ID NO 128; 433pp; English.

XX The invention comprises a method for diagnosing colon cancer in an
 CC individual, the method involves obtaining a serum sample from the
 CC individual and detecting the presence of either TIMP1 or Reg1-alpha and
 CC an additional colorectal cancer-associated marker. The method of the
 CC invention is useful for diagnosing colon cancer in an individual. The
 CC present amino acid sequence represents a human colorectal cancer-
 CC associated protein of the invention.

XX Sequence 175 AA;

Query Match 87.9%; Score 756; DB 8; Length 175;

Best Local Similarity 86.2%; Pred. No. 2.4e-70;

Matches 144; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 YSTEVEAAVNRVLVNLVLRASVYTLISLGFYPRDDVALGVCFFPRLAEKREKREGARLLK 60
 DB 9 YSTDVEAAVNSLVNLVYLQASVYTLISLGFYPRDDVALGVCFFPRLAEKREKREGARLLK 68
 QY 61 MONORGRALFODLOKPSODEWGTTPDAMKAAVLEKSLNQALLDLHALGSKKADPHL 120
 DB 69 MONORGRALFODIKKPADEWGTTPDAMKAAVLEKSLNQALLDLHALGSKKADPHL 128
 QY 121 FLESHFLDEEVKLIKKGMDHLTNLQRLVYSKAGLGEVLFERLLTKHD 167
 DB 129 FLESHFLDEEVKLIKKGMDHLTNLQRLVYSKAGLGEVLFERLLTKHD 175

RESULT 11
 ABM82153
 ID ABM82153 standard; protein; 175 AA.
 AC ABM82153;

PT	18-NOV-2004	(first entry)	
XX			
XX			
DB	Tumour-associated antigenic target (TAT) polypeptide PRO71085, SEQ:5563.		
XX			
XX			
KW	Tumour-associated antigenic target; TAT; human; overexpression; cancer;		
KW	tumour; diagnosis; cell proliferative disorder; breast cancer;		
KW	colorectal cancer; lung cancer; ovarian cancer; liver cancer;		
KW	central nervous system cancer; bladder cancer; pancreatic cancer;		
KW	cervical cancer; melanoma; leukaemia; hybridisation probe;		
KW	chromosome identification; chromosome mapping; gene mapping;		
XX	gene therapy; cytostatic.		
OS			
XX	Homo sapiens.		
PN	WO2004030615-A2.		
PD			
XX	15-APR-2004.		
PD			
XX	29-SEP-2003; 2003WO-US028547.		
PR			
XX	02-OCT-2002; 2002US-041971P.		
PR			
XX	(GETH) GENENTECH INC.		
PA			
XX			
PI	Wu TD, Zhang Z, Zhou Y;		
XX			
DR	WPI, 2004-347921/32.		
DR	N-PsDB; ACN40653.		
XX			
PT			
PT	New tumor-associated antigenic target polypeptides and nucleic acids,		
PT	useful in preparing a medicament for treating or detecting a		
PT	proliferative disorder, e.g. breast, lung, colorectal, ovarian or		
PT	prostate cancer or tumor.		
XX			
PS	Claim 12; SEQ ID NO 5563; 7273pp; English.		
XX			
CC	The invention relates to human tumour-associated antigenic target (TAT)		
CC	polypeptides, and their related nucleic acids. The TAT polypeptides are		
CC	overexpressed in cancer tissues compared to normal tissues, and may thus		
CC	serve as effective targets for the diagnosis and treatment of cancer in		
CC	mammals. The invention also relates to nucleic acid and polypeptide		
CC	sequences at least 80% identical to the TAT nucleic acids and		
CC	polypeptides; expression vectors and host cells comprising a TAT nucleic		
CC	acid; an antibody specific for a TAT polypeptide; a peptide or organic		
CC	molecule which binds to a TAT polypeptide; fusion proteins comprising a		
CC	TAT polypeptide; and methods and compositions for the treatment or		
CC	diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,		
CC	antibodies, antagonists, binding molecules and compositions are useful		
CC	for diagnosing or treating a cell proliferative disorder associated with		
CC	increased TAT expression, particularly cancers such as breast cancer,		
CC	colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder		
CC	cancer, pancreatic cancer, cervical cancer, cancers of the central		
CC	nervous system, melanoma and leukaemia. TAT nucleic acids may further be		
CC	used as hybridisation probes, in chromosome and gene mapping, in		
CC	chromosome identification and in gene therapy. The present sequence		
CC	represents a TAT polypeptide of the invention		
XX			
XX			
SO	Sequence 175 AA;		
	Query Match	87.9%;	Score 756; DB 8; Length 175;
	Best Local Similarity	86.2%;	Pred. No. 2,4e-70;
	Matches 144; Conservative 11; Mismatches 12; Indels 0; Gaps 0		
QY	1 VSTVEAANRLVNLVLTASYYTLSGFPFDRDVALLEGVCHPFEALAEKRGAGRLTK	60	
DB	9 YSTDVAANSLVNLVLTQASYYTLSGFPFDRDVALLEGVSHFPEALAEKRGAGRLTK	68	
QY	61 MONRGGRALFDOLQRPDDEWGTDDAMKAALVLEKSLNQALLDLHALGSKKADPHLC	120	
DB	69 MONRGGRALFDOLQRPDDEWGTDDAMKAALVLEKSLNQALLDLHALGSKKADPHLC	128	
QY	121 FLESHPLEDEVKLIKMGDHLINIQRLVYSKAGLGSLPFRRLTKKD	167	

DB	129 FLETHFLDEBYVTLIKMGDHLNNLRLOGPEAGGEYLFERTLTJLKD 175
XX	RESULT 12
AC	ADB65044 ADB65044 standard; protein; 254 AA.
AD	ADB65044;
AT	04-DEC-2003 (first entry)
CA	Human protein encoded by clone SMINT20016150.
CC	Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration; cell regeneration; membrane protein; signal transduction-related protein; transcription-related protein; osteoporosis; neurological disease; cancer; tumour.
CS	Homo sapiens.
EP	EPI308459-A2.
PD	07-MAY-2003.
PP	28-MAR-2002; 2002EB-00007401.
PR	05-NOV-2001; 2001JP-00379298. 25-JAN-2002; 2002US-00350978.
PA	(HELI-) HELIX RES INST. (REAS-) RES ASSOC BIOTECHNOLOGY.
PI	Isegai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S, Yamamoto J, Isono Y, Hiro Y, Otsuka K, Nagai K, Irle R, Tamechika I, Seki N, Yoshikawa T, Otsuka M, Nagahara K, Masuno Y;
WI	WPI: 2003-450961/43.
N-P	N-PSDB; ADB63074.
PT	New polynucleotides and polypeptides, useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy.
PS	Claim 1; Page; 222pp; English.
XX	The invention discloses a polynucleotide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel polypeptides. Also claimed is a polypeptide encoded by the polynucleotide or its partial peptide, an antibody binding to the polypeptide or peptide of the polynucleotide, immunologically assaying the polypeptide or peptide peptide of the polynucleotide by contacting the polypeptide or peptide with the antibody of the encoded protein, and observing the binding between the two, a transformant carrying the polynucleotide in an expressible manner and an antisense polynucleotide. The oligonucleotide is useful as a primer for synthesising the polynucleotide, or as a probe for detecting the polynucleotide. The polynucleotides and encoded proteins are useful as pharmaceutical agents and many disease-related genes may be included in them, for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy. The genes are involved in tissue and/or cell regeneration. Membrane proteins, signal transduction-related proteins, transcription-related proteins, disease-related proteins and genes encoding them can be used as indicators for diseases (e.g., osteoporosis, neurological diseases, cancer, tumours). The CDNA may be used to regulate the activity or expression of the encoded protein to treat diseases. The sequence presented is a protein of the invention. Note: Some of the sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office.
SQ	Sequence 254 AA;

Query Match	87.9%; Score 756; DB 7; Length 254;
-------------	-------------------------------------

Best Local Similarity 86.2%; Pred. No. 4e-70;
Matches 144; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

```
OY 1 YSTEVEAAVNRLVNLVYLRASTYVLSLGFYFDRDDVALSGVCHFFRELAEBKREGAERLLK 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 88 YSTDVEAAVNSLVNLVYLQASTYVLSLGFYFDRDDVALSGVSHFFRELAEBKREGYERLLK 147
OY 61 MONORGRALFODLQKPSODEWGTTPDAMKAIVLEKSLNQALLDLHALGSKKADPHLCD 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 148 MONORGRALFODIKKPADEWGTTPDAMKAMALEKTLNQALLDLHALGSAKRTDPHLCD 207
OY 121 FLESHFLDEBEVKLIKKGMDHLTNLQRLVYKSKAGLGEYLPERILTAKHD 167
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 208 FLETHFLDEBEVKLIKKGMDHLTNLHRLGPEAGLGEYLPERILTAKHD 254
```

RESULT 13

ADQ82746
ID ADQ82746 standard; protein; 362 AA.

AC ADQ82746;

XX 09-SEP-2004 (first entry)

XX Recombinant human ferritin protein.

XX human; ferritin protein.

XX Homo sapiens.

OS KR2004007892-A.

XX 28-JAN-2004.

XX 11-JUL-2002; 2002KR-00040497.

XX 11-JUL-2002; 2002KR-00040497.

PA (BIOP-) BIOPROGEN CO LTD.

PI Ham MS, Jung BH, Kim SU, Lee EG, Lee JW;

DR WPI; 2004-386312/36.

DR N-Psdb; ADQ82747.

PT New recombinant human ferritin proteins and production method of them.

PS Claim 8; SEQ ID NO 11; 27pp; Korean.

CC The invention comprises the amino acid and coding sequences of a

CC recombinant human ferritin protein, the invention also comprises a

CC production method for the recombinant human ferritin protein. The present

CC amino acid sequence represents the recombinant human ferritin protein of

CC the invention.

CC Sequence 362 AA;

Query Match 87.9%; Score 756; DB 8; Length 362;

Best Local Similarity 86.2%; Pred. No. 6.2e-70;

Matches 144; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

```
OY 1 YSTEVEAAVNRLVNLVYLRASTYVLSLGFYFDRDDVALSGVCHFFRELAEBKREGAERLLK 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 196 YSTDVEAAVNSLVNLVYLQASTYVLSLGFYFDRDDVALSGVSHFFRELAEBKREGYERLLK 255
OY 61 MONORGRALFODLQKPSODEWGTTPDAMKAIVLEKSLNQALLDLHALGSKKADPHLCD 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 256 MONORGRALFODIKKPADEWGTTPDAMKAMALEKTLNQALLDLHALGSAKRTDPHLCD 315
OY 121 FLESHFLDEBEVKLIKKGMDHLTNLQRLVYKSKAGLGEYLPERILTAKHD 167
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 316 FLETHFLDEBEVKLIKKGMDHLTNLHRLGPEAGLGEYLPERILTAKHD 362
```

RESULT 14

AU29923
ID AU29923 standard; protein; 238 AA.

AC AU29923;

XX 18-DEC-2001 (first entry)

DE Novel human secreted protein #414.

XX Human; vaccination; gene therapy; nutritional supplement;

XX stem cell proliferation; haematopoiesis; nerve tissue regeneration;

XX immune suppression; immune stimulation; anti-inflammatory; leukaemia.

OS Homo sapiens.

XX WO200179449-A2.

XX 16-APR-2001; 2001WO-US008656.

XX 18-APR-2000; 2000US-00552929.

XX 26-JAN-2001; 2001US-00770160.

PA (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Drmanac RT;

DR WPI; 2001-611725/70.

PT Nucleic acids encoding a range of human polypeptides, useful in genetic

PT vaccination, testing and therapy.

PS Claim 20; Page 210; 765pp; English.

CC The invention relates to novel human secreted polypeptides. The

CC polypeptides and antibodies to the polypeptides are useful for

CC determining the presence of or predisposition to a disease associated

CC with altered levels of polypeptide. The polypeptides are also useful for

CC identifying agents (agonists and antagonists) that bind to them. Cells

CC expressing the proteins are useful for identifying a therapeutic agent

CC for use in treatment of a pathology related to aberrant expression or

CC physiological interactions of the polypeptide. Vectors comprising the

CC nucleic acids encoding the polypeptides and cells genetically engineered

CC to express them are also useful for producing the proteins. The proteins

CC are useful in genetic vaccination, testing and therapy, and can be used

CC as nutritional supplements. They may be used to increase stem cell

CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon

CC and/or nerve tissue growth or regeneration; immune suppression and/or

CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.

CC AA029510-AA03304 represent the amino acid sequences of novel human

CC secreted proteins of the invention

XX Sequence 238 AA;

Query Match 87.6%; Score 753; DB 4; Length 238;

Best Local Similarity 85.6%; Pred. No. 7.5e-70;

Matches 143; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

```
OY 1 YSTEVEAAVNRLVNLVYLRASTYVLSLGFYFDRDDVALSGVCHFFRELAEBKREGAERLLK 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 72 YSTDVEAAVNSLVNLVYLQASTYVLSLGFYFDRDDVALSGVSHFFRELAEBKREGYERLLK 131
OY 61 MONORGRALFODLQKPSODEWGTTPDAMKAIVLEKSLNQALLDLHALGSKKADPHLCD 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 132 MONORGRALFODIKKPADEWGTTPDAMKAIVLEKSLNQALLDLHALGSAKRTDPHLCD 191
OY 121 FLESHFLDEBEVKLIKKGMDHLTNLQRLVYKSKAGLGEYLPERILTAKHD 167
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 192 FLETHFLDEBEVKLIKKGMDHLTNLHRLGPEAGLGEYLPERILTAKHD 238
```

RESULT 15

AD060419
ID ADO60419 standard; protein; 175 AA.

XX ADO60419;

XX 26-AUG-2004 (first entry)

XX Human ferritin light chain to increase B lymphocyte proliferation.

XX B lymphocyte proliferation; differentiation; maturation; ferritin;

XX diagnosis; HIV infection; lymphoma.

XX Homo sapiens.

XX MO2004045561-A2.

XX 03-JUN-2004.

XX 20-NOV-2003; 2003WO-US037593.

XX 20-NOV-2002; 2002US-0427754P.

XX (UTMA-) UNIV MASSACHUSETTS.

XX Stevenson M, Swingler S;

XX WPI; 2004-431807/40.

XX Inducing B cell proliferation, differentiation or maturation for treating

XX HIV infection or cancer, comprises administering ferritin or a compound

XX that increases ferritin expression or activity to the B cell or its

XX precursor cell.

XX Example 1; SEQ ID NO 1; 86pp; English.

XX The invention relates to a method of increasing at least one of B
CC lymphocyte proliferation, differentiation or maturation, by administering
CC ferritin or a compound that increases ferritin expression or activity to
CC a B lymphocyte or a B lymphocyte precursor cell in an amount to increase
CC B lymphocyte proliferation, differentiation or maturation. The methods
CC are useful for modulating B lymphocyte proliferation, differentiation or
CC maturation, or for identifying compounds that modulate ferritin
CC expression or activity. These may be used for treating or diagnosing HIV
CC infection or lymphoma. This sequence corresponds to the human ferritin
CC light chain protein used in the method of the invention.

XX Sequence 175 AA;

Query Match 86.3%; Score 742; DB 8; Length 175;

Best Local Similarity 85.0%; Pred. No. 7e-69;

Matches 142; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

QY 1 YSTVEAAVNRILVNLIRASYTYLSIGFYPRDDVALBGVCHPFRFLAEKREKGAERLIK 60
DB 9 YSTDVEAAVNRILVNLIRASYTYLSIGFYPRDDVALBGVCHPFRFLAEKREKGAERLIK 68
QY 61 MONORGRALFODLQKPSODEWCTTPDANKAIVLEKSLNOALLDHALGSKKADPHLCD 120
DB 69 MONORGRALFODLQKPSODEWCTTPDANKAIVLEKSLNOALLDHALGSKKADPHLCD 128
QY 121 PLSHPLDEEVKLIKKGDHLTNIQRLVRSKAGLGEYLFERLTCLKHD 167
DB 129 PLSHPLDEEVKLIKKGDHLTNIQRLVRSKAGLGEYLFERLTCLKHD 175

Search completed: August 22, 2005, 09:31:38
Job time : 169 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 22, 2005, 09:06:17 ; Search time 172 Seconds
(without alignments)
497.193 Million cell updates/sec

Title: US-10-617-955-2-COPY
Perfect score: 860
Sequence: 1 YSTEVEAANRLVNLVLRAS.....VKSAAAGLGYLPERLTAKHD 167

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03:.*
1: uniprot_sprot:.*
2: uniprot_trernbl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	839	97.6	174	1 FRIL_HORSE	P02791 equus caball
2	836	87.9	174	1 FRIL_HUMAN	P02792 homo sapien
3	756	87.9	241	2 Q7Z2W1	Q7Z2W1 homo sapien
4	750	87.2	175	2 Q6IBT7	Q6IBT7 homo sapien
5	750	87.2	175	2 Q6SAU9	Q6SAU9 homo sapien
6	748	87.0	175	2 Q6ECU0	Q6ECU0 homo sapien
7	747	86.9	175	2 Q8WU07	Q8WU07 homo sapien
8	745	86.6	175	2 Q86W19	Q86W19 homo sapien
9	745	86.6	175	2 Q9JYM8	Q9JYM8 cavia porce
10	738	85.8	174	1 FRIL_BOVIN	Q46415 bos taurus
11	738	85.8	174	1 FRIL_RABIT	P09451 coryctolagus
12	731	85.0	175	2 Q9BYW6	Q9BYW6 homo sapien
13	731	85.0	175	2 Q9JYK6	Q9JYK6 cavia porce
14	728	84.7	183	2 Q6P7T1	Q6P7T1 ractus norv
15	726	84.4	182	1 FRIL_RAT	P02793 ractus norv
16	721	83.8	182	1 FRIL_MOUSE	P49945 mus musculu
17	716	83.3	183	2 Q9CPX4	Q9CPX4 m mus muscu
18	712	82.8	182	1 FRIL_MOUSE	P29391 mus musculu
19	712	82.8	183	2 Q66GWO	Q66GWO xenopus lae
20	709	82.4	191	2 Q6S4P3	Q6S4P3 homo sapien
21	673	78.3	160	2 Q9GLB7	Q9GLB7 sus scrofa
22	595.5	69.2	1310	2 Q7TP54	Q7TP54 ractus norv
23	538	62.6	178	2 Q6P4N0	Q6P4N0 xenopus tro
24	536	62.3	176	2 Q6P8C6	Q6P8C6 xenopus tro
25	535	62.2	176	1 FRIL_RANCA	P07229 rana catesb
26	534	62.1	178	2 Q7ZMW3	Q7ZMW3 xenopus lae
27	532	61.9	173	2 Q6DFP5	Q6DFP5 xenopus tro
28	530	61.6	177	1 FRIL_XENLA	Q78A55 xenopus lae
29	529	61.4	177	2 Q801J5	Q801J5 petromyzon
30	528	61.4	176	2 Q6PAB7	Q6PAB7 xenopus lae
31	526	61.2	177	2 Q6P653	Q6P653 xenopus lae

32	523	60.8	176	2 P79821	P79821 oncorhynch
33	521	60.6	176	2 P79823	P79823 oncorhynch
34	520	60.5	176	2 P79822	P79822 oncorhynch
35	518	60.2	176	1 FRIL_XENLA	P17653 xenopus lae
36	516	60.0	176	1 FRIL_XENLA	P49947 salmo salar
37	514	59.8	176	1 FRIL_XENLA	P49948 xenopus lae
38	513	59.7	176	1 FRIL_XENLA	P07798 rana catesb
39	498	57.9	177	2 Q6DD55	Q6DD55 xenopus tro
40	498	57.9	177	2 Q6DD55	Q6DD55 xenopus tro
41	498	57.9	182	2 Q920K4	Q920K4 cavia porce
42	497	57.8	177	2 Q7ZXM8	Q7ZXM8 xenopus lae
43	497	57.8	182	2 Q8M1P0	Q8M1P0 equus caball
44	496	57.7	174	2 Q6DHT8	Q6DHT8 brachydanio
45	495	57.6	177	1 FRIL_XENLA	Q78A55 xenopus lae

ALIGNMENTS

RESULT 1
FRIL_HORSE STANDARD, PRT, 174 AA.
ID FRIL_HORSE
AC P02791;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ferritin light chain (Ferritin L subunit).
GN Name=FTL;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93363645; PubMed=8357841; DOI=10.1016/0167-4781(93)90121-S;
RA Takeda S., Ohta M., Ebina S., Nagayama K.;
RT "Cloning, expression and characterization of horse L-ferritin in
RT Escherichia coli.";
RL Biochim. Biophys. Acta 1174:218-220(1993).
RN (2)
RP SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=82027739; PubMed=7026284; DOI=10.1016/0014-5793(81)80193-7;
RA Heutsdpreute M., Crichton R.R.;
RT "Amino acid sequence of horse spleen apoferritin.";
RL FEBS Lett. 129:322-327(1981).
RN (3)
RP SEQUENCE.
RC TISSUE=Liver;
RA Mathijs J.M., Crichton R.R.;
RT "Amino acid sequence of horse liver ferritin.";
RL S. Afr. J. Sci. 80:424-426(1984).
RN (4)
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RX MEDLINE=81052459; PubMed=7432529;
RA Clegg G.A., Stanfield R.F.D., Bourne P.E., Harrison P.M.;
RT "Helix packing and subunit conformation in horse spleen apoferritin.";
RL Nature 288:298-300(1980).
RN (5)
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RX PubMed=15299370;
RA Precigoux G., Yaviv J., Gallois B., Dautant A., Courseville C.,
D'Estainot B.L.;
RT "A crystallographic study of haem binding to ferritin.";
RL Acta Crystallogr. D 50:739-743(1994).
RN (6)
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=97303050; PubMed=9159481; DOI=10.1006/jmbi.1997.0970;
RA Hemstead P.D., Yewdall S.J., Fernie A.R., Lawson D.M., Artyukh P.J.,
Rice D.W., Ford G.C., Harrison P.M.;
RT "Comparison of the three-dimensional structures of recombinant human H
and horse L ferritins at high resolution.";

RL J. Mol. Biol. 268:424-448(1997).
 CC - FUNCTION: Ferritin is an intracellular molecule that stores iron
 CC in a soluble, nontoxic, readily available form. The functional
 CC molecule, which is composed of 24 chains, is roughly spherical and
 CC contains a central cavity into which the polymeric ferric iron
 CC core is deposited.
 CC - MISCELLANEOUS: There are two types of ferritin subunits: L (light)
 CC chain and H (heavy) chain. The major chain can be light or heavy,
 CC depending on the species and tissue type.
 CC - MISCELLANEOUS: In horse spleen the light chain is the major chain.
 CC - SIMILARITY: Belongs to the ferritin family.
 CC - SIMILARITY: Contains 1 ferritin-like diron domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL, D14523, BAA03396.1; -
 CC PIR, S36118, FRHOL.
 CC DR PDB, 1AEW; X-ray; @=1-174.
 CC DR PDB, 1DAT; X-ray; @=1-174.
 CC DR PDB, 1GMG; X-ray; A=1-174.
 CC DR PDB, 1HRS; X-ray; @=1-174.
 CC DR PDB, 1IER; X-ray; @=1-174.
 CC DR PDB, 1IES; X-ray; A/B/C/D/E/F=1-174.
 CC DR InterPro: IPR001519; Ferritin.
 CC DR InterPro: IPR009078; Ferritin Dps.
 CC DR InterPro: IPR008331; Ferritin.
 CC DR InterPro: IPR009040; Ferritin-like.
 CC DR Pfam: PF00210; Ferritin_1.
 CC DR Pfam: PF000971; Ferritin_1.
 CC DR PROSITE: PS00540; FERRITIN_1; 1.
 CC DR PROSITE: PS00204; FERRITIN_2; 1.
 CC DR PROSITE: PS50905; FERRITIN LIKE; 1.
 CC KW 3D-structure; Acetylation; Direct protein sequencing; Iron;
 CC Iron storage; Metal-binding.
 CC FT INIT MET 0
 CC FT DOMAIN 6 155 Ferritin-like diron.
 CC FT MOD RES 1 1 Catalytic site for iron oxidation.
 CC FT METAL 53 53 Iron (Potential).
 CC FT METAL 56 56 Iron (Potential).
 CC FT METAL 57 57 Iron (Potential).
 CC FT METAL 60 60 Iron (Potential).
 CC FT METAL 63 63 Iron (Potential).
 CC FT CONFLICT 93 93 P -> L (in Ref. 2 and 3).
 CC FT CONFLICT 135 137 DBE -> NEQ (in Ref. 3).
 CC FT HELIX 10 36
 CC FT TURN 37 38
 CC FT TURN 40 42
 CC FT HELIX 45 72
 CC FT TURN 73 73
 CC FT HELIX 92 120
 CC FT TURN 121 121
 CC FT HELIX 123 132
 CC FT TURN 133 133
 CC FT HELIX 134 157
 CC FT HELIX 159 169
 CC FT TURN 170 170
 CC SEQUENCE 174 AA; 19830 MW; AE039CA1BD046D4F CRC64;
 Query Match 97.6%; Score 839; DB 1; Length 174;
 Best Local Similarity 97.6%; Pred. No. 7.5e-62;
 Matches 163; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 61 MONORGRALFODLOKESODEWGTTPDAMKAATVLEKSLNQAALDLHALGSKKADPHLCD 120
 Db 68 MONORGRALFODLOKESODEWGTTPDAMKAATVLEKSLNQAALDLHALGSKKADPHLCD 127
 Oy 121 FLESHFLDEEVKLIKXMGDHLTNIOQLVNSAGIGEVLFERLTUKHD 167
 Db 128 FLESHFLDEEVKLIKXMGDHLTNIOQLVNSAGIGEVLFERLTUKHD 174
 RESULT 2
 ID FRIL HUMAN STANDARD; PRT; 174 AA.
 AC P02792; Q9B728;
 DT 21-JUN-1986 (Rel. 01, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Ferritin light chain (ferritin L subunit).
 GN Name=FTL;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86176772; PubMed=3754330;
 RA Santoro C, Marone M, Ferrone M, Costanzo F, Colombo M,
 RA Minganti C, Cortese R, Silengo L;
 RT "Cloning of the gene coding for human L apoferritin."
 RL Nucleic Acids Res. 14:2863-2876(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=65216457; PubMed=3858810;
 RA Dörner M.H., Salfield J., Will H., Leibold E.A., Vass J.K., Munro H.N.;
 RT "Structure of human ferritin light subunit messenger RNA: comparison
 RT with heavy subunit message and functional implications."
 RL Proc. Natl. Acad. Sci. U.S.A. 82:3139-3143(1985).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=66088223; PubMed=3840162;
 RA Boyd D., Vecoli C., Belcher D.M., Jain S.K., Drysdale J.W.;
 RT "Structural and functional relationships of human ferritin H and L
 RT chains deduced from cDNA clones."
 RL J. Biol. Chem. 260:11755-11761(1985).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Brain, Skin, and Urinary bladder;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Tosiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek A., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.U.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP SEQUENCE OF 32-174 FROM N.A.
 RX MEDLINE=87064341; PubMed=3023856;
 RA Chou C.-C., Gatti R.A., Fuller M.L., Concannon P., Wong A., Chada S.,
 RA Davis R.C., Salsner W.A.;
 RT "Structure and expression of ferritin genes in a human promyelocytic

cell line that differentiates in vitro.";
 RL Mol. Cell. Biol. 6:566-573(1986).
 RP SEQUENCE OF 1-35 AND 40-174.
 RC TISSUE=Liver;
 RX MEDLINE=84085077; PubMed=6653779; DOI=10.1016/0014-5793(83)90037-4;
 RA Addison J.M., Filson J.E., Lewis W.G., May K., Harrison P.M.;
 RT "The amino acid sequence of human liver apoferritin.";
 RL FEBS Lett. 164:139-144(1983).
 RN [7]
 RP SEQUENCE OF 83-89 AND 144-154.
 RC TISSUE=Placenta;
 RX PubMed=8706693;
 RA Vladimirov S.N., Ivanov A.V., Karpova G.G., Musolyamov A.K.,
 RT Egorov T.A., Thiede B., Wittmann-Liebold B., Otto A.;
 RL "Characterization of the human small-ribosomal-subunit proteins by N-terminal and internal sequencing, and mass spectrometry.";
 CC Eur. J. Biochem. 239:144-149(1996).
 CC -1- FUNCTION: Ferritin is an intracellular molecule that stores iron in a soluble, nontoxic, readily available form. The functional molecule, which is composed of 24 chains, is roughly spherical and contains a central cavity into which the polymeric ferric iron core is deposited.
 CC -1- MISCELLANEOUS: There are two types of ferritin subunits: L (light) chain and H (heavy) chain. The major chain can be light or heavy, depending on the species and tissue type.
 CC -1- SIMILARITY: Belongs to the ferritin family.
 CC -1- SIMILARITY: Contains 1 ferritin-like diron domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation- the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL, M11147; AAA52439.1; -;
 CC EMBL, M10119; AAA55831.1; -;
 CC EMBL, M12938; AAA52440.1; -;
 CC EMBL, BC002991; AAH02991.2; -;
 CC EMBL, BC004245; AAH04245.1; -;
 CC EMBL, BC008439; AAH08439.1; -;
 CC EMBL, BC016346; AAH16346.1; -;
 CC EMBL, BC016354; AAH16354.1; -;
 CC EMBL, BC018990; AAH18990.1; -;
 CC EMBL, BC058820; AAH58820.1; -;
 CC EMBL, X03742; CAA27382.1; -;
 CC EMBL, X03743; CAA27383.1; -;
 CC EMBL, X03743; CAA27384.1; -;
 CC PIR, B23920; PRHUL.
 CC HSSP, P29391; 1LB3.
 CC DR Genew, HGNC:3999; PTL.
 CC H-INDB; HIK0015310; -;
 CC MIM, 134790; -;
 CC DR GO; GO:0008043; C:ferritin complex; TAS.
 CC DR GO; GO:0005506; P:iron ion binding; TAS.
 CC DR GO; GO:0006879; P:iron ion homeostasis; TAS.
 CC DR InterPro; IPR001519; Ferritin.
 CC DR InterPro; IPR009078; Ferritin/RR_like.
 CC DR InterPro; IPR008331; Ferritin_Dps.
 CC DR InterPro; IPR009040; Ferritin_like.
 CC DR Pfam; PF00210; Ferritin; 1.
 CC DR Prodom; PD000971; Ferritin; 1.
 CC DR PROSITE; PS00540; FERRITIN_1; 1.
 CC DR PROSITE; PS00204; FERRITIN_2; 1.
 CC DR PROSITE; PS00905; FERRITIN_LIKE; 1.
 CC DR Acetylation; Direct protein sequencing; Iron; Iron storage;
 CC KM Metal-binding.
 CC FT INIT MET 0 0
 CC FT DOMAIN 6 155 Ferritin-like diron.
 CC FT DOMAIN 53 60 Catalytic site for iron oxidation.
 CC FT MOD_RES 1 1 N-acetylsuccinate.

FT METAL 53 53 Iron (Potential).
 FT METAL 56 56 Iron (Potential).
 FT METAL 57 57 Iron (Potential).
 FT METAL 60 60 Iron (Potential).
 FT METAL 63 63 Iron (Potential).
 FT CONFLICT 53 53 E -> Q (in Ref. 5).
 FT CONFLICT 86 86 E -> Q (in Ref. 5).
 FT CONFLICT 88 88 E -> W (in Ref. 7).
 FT CONFLICT 101 101 A -> T (in Ref. 2).
 FT CONFLICT 153 153 R -> A (in Ref. 7).
 FT CONFLICT 174 174 D -> N (in Ref. 5).
 SQ SEQUENCE 174 AA; 19888 MW; 8F0B4B23B6CAFEF2 CRC64;
 Query Match 87.9%; Score 756; DB 1; Length 174;
 Best Local Similarity 86.2%; Pred. No. 5.9e-55;
 Matches 144; Conservative 11; Mismatches 12; Indels 0; Gaps 0;
 QY 1 YSTEVEAAVNLVNLVYLKASYTSLGFFPDRDVALGCVHPFRELAEKREGARLLK 60
 DB 8 YSTDVEAAVNLVNLVYLQASTYLSLGFYFDRDVALGCVHPFRELAEKREGYERLLK 67
 QY 61 MONRGGRALFODLQKPSQDEWGTTPDMKAAIVLEKSLNALDLHALGSKADPHLCD 120
 DB 68 MONRGGRALFODIKKPADEWGTTPDMKAAIALEKSLNALDLHALGSRTPHLCD 127
 QY 121 FLESHFLDEEYKLTIKMGDHLTNIORLYKSNAGSEYLFERLTLLKHD 167
 DB 128 FLESHFLDEEYKLTIKMGDHLTNIORLYKSNAGSEYLFERLTLLKHD 174
 RESULT 3
 ID Q722M1 PRELIMINARY; PRT; 241 AA.
 AC Q722M1;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein DKFZp686L19147 (Fragment).
 GN Name=DKFZp686L19147;
 OS Homo sapiens (Human);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Human colon endochel primary cell culture;
 RG The German Human CDNA Consortium;
 RA Koehler K., Beyer A., Mewes H.W., Well B., Amid C., Oeanger A.,
 RL Fobo G., Han M., Wiemann S.;
 CC Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Ferritin is an intracellular molecule that stores iron in a soluble, nontoxic, readily available form. The functional molecule, which is composed of 24 chains, is roughly spherical and contains a central cavity into which the polymeric ferric iron core is deposited (By similarity).
 CC -1- SIMILARITY: Belongs to the ferritin family.
 CC -1- SIMILARITY: Contains 1 ferritin-like diron domain.
 CC EMBL, BX571748; CAB11873.1; -;
 CC DR HSSP; P02791; IGWG.
 CC DR GO; GO:0005488; P:binding; IEA.
 CC DR GO; GO:0008199; P:ferric iron binding; IEA.
 CC DR GO; GO:0006879; P:iron ion homeostasis; IEA.
 CC DR GO; GO:0006826; P:iron ion transport; IEA.
 CC DR InterPro; IPR001519; Ferritin.
 CC DR InterPro; IPR009078; Ferritin/RR_like.
 CC DR InterPro; IPR008331; Ferritin_Dps.
 CC DR InterPro; IPR009040; Ferritin_like.
 CC DR Pfam; PF00210; Ferritin; 1.
 CC DR Prodom; PD000971; Ferritin; 1.
 CC DR PROSITE; PS00540; FERRITIN_1; 1.
 CC DR PROSITE; PS00204; FERRITIN_2; 1.
 CC DR PROSITE; PS00905; FERRITIN_LIKE; 1.
 CC DR Hypothetical protein; Iron; Iron storage; Metal-binding.


```
CC contains a central cavity into which the polymeric ferric iron
CC core is deposited (By similarity).
CC -1- SIMILARITY: Belongs to the ferritin family.
CC -1- SIMILARITY: Contains 1 ferritin-like diiron domain.
DR EMBL: BC021670; AAH21670.1; -.
DR HSSP: P29391; 1LB3.
DR GO: GO:0005488; F:binding; IEA.
DR GO: GO:0008199; F:ferric iron binding; IEA.
DR GO: GO:0006879; P:iron ion homeostasis; IEA.
DR GO: GO:0006826; P:iron ion transport; IEA.
DR Pfam: PF00210; Ferritin; 1.
DR ProDom: PD000971; Ferritin; 1.
DR PROSITE: PS00540; FERRITIN_1; 1.
DR PROSITE: PS00204; FERRITIN_2; 1.
DR PROSITE: PS50905; FERRITIN_LIKE; 1.
KW Iron; Iron storage; Metal-Binding.
SQ SEQUENCE 175 AA; 20662 MW; 18ADDD1DBA8C6A69 CRC64;

Query Match      86.9%; Score 747; DB 2; Length 175;
Best Local Similarity 85.6%; Pred. No. 3,3e-54;
Matches 143; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 1 YSTEVEAANVRNLVNLVYLRASYTYSLSGFYFDRDVALGEGVCHFFRELAEEKREGAERLLK 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 9 YSTDVEAANVNSLVNLVYLGASTYYSLSGFYFDRDVALGEGVSHFFRELAEEKREGYERLLK 68
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 MONORGGRALFODLQKPSQDEWGTTPDAMKAIVLEKSLNQALDLHALGSKKADPHLCD 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 69 MONQVGRALFODIKKPADEWEGKTPDAMKAAMALEKLNQALDLHALGSAHRTDPHLCD 128
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 121 FLESHFLDEEVYLLKKMGDHLTNIQRLVSKAGLGEYLFERLTLLKHD 167
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 129 FLETHFLDEEVYLLKKMGDHLTNLHRLGSPGAGLGEYLFERLTLLKHD 175
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 8
Q86WI9 PRELIMINARY; PRT; 175 AA.
ID Q86WI9;
AC Q86WI9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ferritin-like protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Li X., Obunike J., Tilson M.D.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
CC -1- FUNCTION: Ferritin is an intracellular molecule that stores iron
CC in a soluble, nontoxic, readily available form. The functional
CC molecule, which is composed of 24 chains, is roughly spherical and
CC contains a central cavity into which the polymeric ferric iron
CC core is deposited (By similarity).
CC -1- SIMILARITY: Belongs to the ferritin family.
CC -1- SIMILARITY: Contains 1 ferritin-like diiron domain.
DR EMBL: AY207005; AAOS2739.1; -.
DR HSSP: P29391; 1LB3.
DR GO: GO:0005488; F:binding; IEA.
DR GO: GO:0008199; F:ferric iron binding; IEA.
DR GO: GO:0006879; P:iron ion homeostasis; IEA.
DR GO: GO:0006826; P:iron ion transport; IEA.
DR InterPro: IPR001519; Ferritin.
DR InterPro: IPR009078; Ferritin/RR like.
DR InterPro: IPR008331; Ferritin Dps.
DR InterPro: IPR009040; Ferritin_like.
DR Pfam: PF00210; Ferritin; 1.
DR ProDom: PD000971; Ferritin; 1.
DR PROSITE: PS00540; FERRITIN_1; 1.
DR PROSITE: PS00204; FERRITIN_2; 1.
DR PROSITE: PS50905; FERRITIN_LIKE; 1.
```

```
KW Iron; Iron storage; Metal-binding.
SQ SEQUENCE 175 AA; 19986 MW; 615966FF5932F82 CRC64;

Query Match      86.6%; Score 745; DB 2; Length 175;
Best Local Similarity 85.0%; Pred. No. 4.8e-54;
Matches 142; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

QY 1 YSTEVEAANVRNLVNLVYLRASYTYSLSGFYFDRDVALGEGVCHFFRELAEEKREGAERLLK 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 9 YSTDVEAANVDELVNLVYLGASTYYSLSGFYFDRDVALGEGVSHFFRELAEEKREGYERLLK 68
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 MONORGGRALFODLQKPSQDEWGTTPDAMKAIVLEKSLNQALDLHALGSKKADPHLCD 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 69 MONORGGRALFODIKKPADEWEGKTPDAMKAAMALEKLNQALDLHALGSAHRTDPHLCD 128
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 121 FLESHFLDEEVYLLKKMGDHLTNIQRLVSKAGLGEYLFERLTLLKHD 167
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 129 FLETHFLDEEVYLLKKMGDHLTNLHRLGSPGAGLGEYLFERLTLLKHD 175
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 9
Q9JRM8 PRELIMINARY; PRT; 175 AA.
ID Q9JRM8;
AC Q9JRM8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ferritin light chain.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20218664; Pubmed=10753629; DOI=10.1006/dbrc.2000.2425;
RA Cheng Q., Gonzalez P., Zigler J.S. Jr.;
RT "High level of ferritin light chain mRNA in lens.";
RL Biochem. Biophys. Res. Commun. 270:349-355(2000).
CC -1- FUNCTION: Ferritin is an intracellular molecule that stores iron
CC in a soluble, nontoxic, readily available form. The functional
CC molecule, which is composed of 24 chains, is roughly spherical and
CC contains a central cavity into which the polymeric ferric iron
CC core is deposited (By similarity).
CC -1- SIMILARITY: Belongs to the ferritin family.
CC -1- SIMILARITY: Contains 1 ferritin-like diiron domain.
DR EMBL: AF233445; AAF36408.1; -.
DR PIR: JC7238; JC7238.
DR HSSP: P02791; 1GMG.
DR GO: GO:0005488; F:binding; IEA.
DR GO: GO:0008199; F:ferric iron binding; IEA.
DR GO: GO:0006879; P:iron ion homeostasis; IEA.
DR GO: GO:0006826; P:iron ion transport; IEA.
DR InterPro: IPR001519; Ferritin.
DR InterPro: IPR009078; Ferritin/RR like.
DR InterPro: IPR008331; Ferritin Dps.
DR InterPro: IPR009040; Ferritin_like.
DR Pfam: PF00210; Ferritin; 1.
DR ProDom: PD000971; Ferritin; 1.
DR PROSITE: PS00540; FERRITIN_1; 1.
DR PROSITE: PS00204; FERRITIN_2; 1.
DR PROSITE: PS50905; FERRITIN_LIKE; 1.
KW Iron; Iron storage; Metal-binding.
SQ SEQUENCE 175 AA; 19944 MW; 2BC53200ADE4E109 CRC64;

Query Match      86.6%; Score 745; DB 2; Length 175;
Best Local Similarity 85.6%; Pred. No. 4.8e-54;
Matches 143; Conservative 14; Mismatches 10; Indels 0; Gaps 0;

QY 1 YSTEVEAANVRNLVNLVYLRASYTYSLSGFYFDRDVALGEGVCHFFRELAEEKREGAERLLK 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 9 YSTEVEAANVRNLVNLVYLGASTYYSLSGFYFDRDVALGEGVSHFFRELAEEKREGAERLLK 68
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 MONORGGRALFODLQKPSQDEWGTTPDAMKAIVLEKSLNQALDLHALGSKKADPHLCD 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```

Db      69 MONORGGALFODVQKPSDEMGKTLDMEMALTLTKSLNALDLHALGSAKTDPRVCD 128
Oy      121 FLESHFLDEEVKLIKMGDHLTNLQRLVKSAGIGELYFERLTUKHD 167
Db      129 FLESHFLDEEVKLIKMGDHLTNLRLRLLGPPAGIGELYFERLTUKHD 175

RESULT 10
FRIL_BOVIN
ID FRIL_BOVIN STANDARD; PRT; 174 AA.
AC 046415;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ferritin light chain (Ferritin L subunit).
GN Name=FTL;
OS Bos taurus (Bovine); Chordata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=98129059; PubMed=9467878; DOI=10.1016/S0305-0491(97)00277-0;
RA Orlino K., Eguuchi K., Nakayama T., Yamamoto S., Matsunabe K.;
RT "Sequencing of cDNA clones that encode bovine ferritin H and L
   chains."
RT Comp. Biochem. Physiol. 118B:667-673(1997).
CC -1- FUNCTION: Ferritin is an intracellular molecule that stores iron
   in a soluble, nontoxic, readily available form. The functional
   molecule, which is composed of 24 chains, is roughly spherical and
   contains a central cavity into which the polymeric ferric iron
   core is deposited.
CC -1- MISCELLANEOUS: There are two types of ferritin subunits: L (light)
   chain and H (heavy) chain. The major chain can be light or heavy,
   depending on the species and tissue type.
CC -1- SIMILARITY: Belongs to the ferritin family.
CC -1- SIMILARITY: Contains 1 ferritin-like diiron domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
   between the Swiss Institute of Bioinformatics and the EMBL outstation-
   CC the European Bioinformatics Institute. There are no restrictions on its
   use by non-profit institutions as long as its content is in no way
   modified and this statement is not removed. Usage by and for commercial
   CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
   or send an email to license@isb-sib.ch).
CC -----
CC EMBL, AB003094; BAA24819.1; -.
DR HSSP, P02791; IGMG.
DR InterPro, IPR001519; Ferritin.
DR InterPro, IPR009078; Ferritin/RR_like.
DR InterPro, IPR008331; Ferritin_Dps.
DR InterPro, IPR009040; Ferritin_like.
DR Pfam, PF00210; Ferritin; 1.
DR ProDom, PD000971; Ferritin; 1.
DR PROSITE, PS00540; FERRITIN_1; 1.
DR PROSITE, PS00204; FERRITIN_2; 1.
DR PROSITE, PS00905; FERRITIN_LIKE; 1.
DR Iron; Iron storage; Metal-binding.
DR Iron; Iron storage; Metal-binding.
FT INIT MET 0 0
FT DOMAIN 6 155 By similarity.
FT METAL 53 53 Ferritin-like diiron.
FT METAL 56 56 Iron (Potential).
FT METAL 57 57 Iron (Potential).
FT METAL 57 57 Iron (Potential).
FT METAL 60 60 Iron (Potential).
FT METAL 63 63 Iron (Potential).
SQ SEQUENCE 174 AA; 19856 MW; C5SD03F9F8D05C48 CRC64;

Query Match 85.8%; Score 738; DB 1; Length 174;
Best Local Similarity 83.8%; Pred. No. 1.8e-53;
Matches 140; Conservative 15; Mismatches 12; Indels 0; Gaps 0;

```

```

Oy      1 YSTEVEAANRLVNLVRASATYLSLGFYFDRDDVALEGVCHFRRLAEKREGAERLLK 60
Db      8 YSTEVEAANRLVNLVNLVNLVNLVNLVNLVNLVNLVNLVNLVNLVNLVNLVNLVNL 67
Oy      61 MONORGGALFODVQKPSDEMGKTPDAMKAATVLEKSLNALDLHALGSAKADPHICD 120
Db      68 LQNRGGALFLDVQKPSDEMGKTPDAMEALLVEKSLNALDLHALGSAKADPHICD 127
Oy      121 FLESHFLDEEVKLIKMGDHLTNLQRLVKSAGIGELYFERLTUKHD 167
Db      128 FLESHFLDEEVKLIKMGDHLTNLRLRLLGPPAGIGELYFERLTUKHD 174

RESULT 11
FRIL_RABIT
ID FRIL_RABIT STANDARD; PRT; 174 AA.
AC P09451;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ferritin light chain (Ferritin L subunit).
GN Name=FTL;
OS Oryctolagus cuniculus (Rabbit);
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OC NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=New Zealand white; TISSUE=Liver;
RX MEDLINE=88319979; PubMed=3412911;
RA Daniels-McQueen S., Ray A., Walden W.E., Ray B.K., Brown P.H.,
   Thach K.E.;
RT "Nucleotide sequence of cDNA encoding rabbit ferritin L chain."
RT Nucleic Acids Res. 16:7741-7741(1988).
CC -1- FUNCTION: Ferritin is an intracellular molecule that stores iron
   in a soluble, nontoxic, readily available form. The functional
   molecule, which is composed of 24 chains, is roughly spherical and
   contains a central cavity into which the polymeric ferric iron
   core is deposited.
CC -1- MISCELLANEOUS: There are two types of ferritin subunits: L (light)
   chain and H (heavy) chain. The major chain can be light or heavy,
   depending on the species and tissue type.
CC -1- SIMILARITY: Belongs to the ferritin family.
CC -1- SIMILARITY: Contains 1 ferritin-like diiron domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
   between the Swiss Institute of Bioinformatics and the EMBL outstation-
   CC the European Bioinformatics Institute. There are no restrictions on its
   use by non-profit institutions as long as its content is in no way
   modified and this statement is not removed. Usage by and for commercial
   CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
   or send an email to license@isb-sib.ch).
CC -----
CC EMBL, X07830; CA30682.1; -.
DR PIR, S01239; S01239.
DR HSSP, P29391; ILB3.
DR InterPro, IPR001519; Ferritin.
DR InterPro, IPR009078; Ferritin/RR_like.
DR InterPro, IPR008331; Ferritin_Dps.
DR InterPro, IPR009040; Ferritin_like.
DR Pfam, PF00210; Ferritin; 1.
DR ProDom, PD000971; Ferritin; 1.
DR PROSITE, PS00540; FERRITIN_1; 1.
DR PROSITE, PS00204; FERRITIN_2; 1.
DR PROSITE, PS00905; FERRITIN_LIKE; 1.
DR Iron; Iron storage; Metal-binding.
DR Iron; Iron storage; Metal-binding.
FT INIT MET 0 0
FT DOMAIN 6 155 By similarity.
FT METAL 53 53 Ferritin-like diiron.
FT METAL 56 56 Iron (Potential).
FT METAL 57 57 Iron (Potential).
FT METAL 60 60 Iron (Potential).

```

```
FT METAL 63 63 Iron (Potential).
SQ SEQUENCE 174 AA; 19943 MW; B9B03050B233BB86 CRC64;

Query Match 85.8%; Score 738; DB 1; Length 174;
Best Local Similarity 85.6%; Pred. No. 1.8e-53;
Matches 143; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 1 YSTEVEAAVNRVLVNLVLRASVYLSLGFYFDRDDVALGVCHFFRELAEKREGAERLLK 60
DB 8 YSPEVEAAVNRVLVNLVLRASVYLSLGFYFDRDDVALGVSHFFRELAEKREAERLLK 67

QY 61 MONORGRALFODLQKPSODEWGTTPDAMKAALVLEKSLNQALLDLHALGSKKADPHLCD 120
DB 68 MONORGRALFODVQKPSODEWGTTLNMEKALALEKLNQALLDLHALGSHNDPHLCD 127

QY 121 FLESHFLDEEVKLIKKGMDHLTNIRLVKSKAGLGEYLFERLTLKHD 167
DB 128 FLESHFLDEEVKLIKKGMDHLTNIRLVKSGPQASLGEYLFERLTLKHD 174

RESULT 12
Q9BYW6 PRELIMINARY; PRT; 175 AA.
AC Q9BYW6;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Df68IN20.2 (Novel protein similar to ferritin, light polypeptide (FTL)).
GN Name=dJ68IN20.2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith M.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Ferritin is an intracellular molecule that stores iron
CC in a soluble, nontoxic, readily available form. The functional
CC molecule, which is composed of 24 chains, is roughly spherical and
CC contains a central cavity into which the polymeric ferric iron
CC core is deposited (By similarity).
CC -1- SIMILARITY: Belongs to the ferritin family.
CC -1- SIMILARITY: Contains 1 ferritin-like diron domain.
CC EMBL; AL031670; CAB43181.1; -.
DR HSSP; P29391; 1LB3.
DR GeneW; HGNC:4000; FTL1.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR InterPro; IPR001519; Ferritin.
DR InterPro; IPR009078; Ferritin/RR like.
DR InterPro; IPR008331; Ferritin Dps.
DR InterPro; IPR009040; Ferritin_Like.
DR Pfam; PF00210; Ferritin_1.
DR ProDom; PD000971; Ferritin_1.
DR PROSITE; PS00540; FERRITIN_1; 1.
DR PROSITE; PS00204; FERRITIN_2; 1.
DR PROSITE; PS00905; FERRITIN_LIKE; 1.
KW Iron; Iron storage; Metal-binding.
SQ SEQUENCE 175 AA; 20075 MW; ECCCB0AFL09F8BD CRC64;

Query Match 85.0%; Score 731; DB 2; Length 175;
Best Local Similarity 84.3%; Pred. No. 7e-53;
Matches 140; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 1 YSTEVEAAVNRVLVNLVLRASVYLSLGFYFDRDDVALGVCHFFRELAEKREGAERLLK 60
DB 9 YSTEVEAAVNRVLVNLVLRASVYLSLGFYFDRDDVALGVSHFFRELAEKREAERLLK 68

QY 61 MONORGRALFODLQKPSODEWGTTPDAMKAALVLEKSLNQALLDLHALGSKKADPHLCD 120
DB 68 MONORGRALFODVQKPSODEWGTTLNMEKALALEKLNQALLDLHALGSHNDPHLCD 127
```

```
DB 69 MONORGRALFODIKKPADEWGTTPDAMKAAMALEKLNQALLDLHALGSHNDPHLCD 128
QY 121 FLESHFLDEEVKLIKKGMDHLTNIRLVKSKAGLGEYLFERLTLKHD 166
DB 129 FLESHFLDEEVKLIKKGMDHLTNIRLVKSGPEAGLGEYLFERLTLKHD 174

RESULT 13
Q9UKP6 PRELIMINARY; PRT; 175 AA.
AC Q9UKP6;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Ferritin light chain.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RA Seyoz C.; Buronfosse T.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Ferritin is an intracellular molecule that stores iron
CC in a soluble, nontoxic, readily available form. The functional
CC molecule, which is composed of 24 chains, is roughly spherical and
CC contains a central cavity into which the polymeric ferric iron
CC core is deposited (By similarity).
CC -1- SIMILARITY: Belongs to the ferritin family.
CC EMBL; AF230928; AAF68948.1; -.
DR HSSP; P02791; 1GMG.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR InterPro; IPR001519; Ferritin.
DR InterPro; IPR009078; Ferritin/RR like.
DR InterPro; IPR008331; Ferritin Dps.
DR InterPro; IPR009040; Ferritin_Like.
DR Pfam; PF00210; Ferritin_1.
DR ProDom; PD000971; Ferritin_1.
DR PROSITE; PS00540; FERRITIN_1; 1.
DR PROSITE; PS00204; FERRITIN_2; 1.
DR PROSITE; PS00905; FERRITIN_LIKE; 1.
KW Iron; Iron storage; Metal-binding.
SQ SEQUENCE 175 AA; 19904 MW; 85FDDCD31546696A CRC64;

Query Match 85.0%; Score 731; DB 2; Length 175;
Best Local Similarity 84.4%; Pred. No. 7e-53;
Matches 141; Conservative 14; Mismatches 12; Indels 0; Gaps 0;

QY 1 YSTEVEAAVNRVLVNLVLRASVYLSLGFYFDRDDVALGVCHFFRELAEKREGAERLLK 60
DB 9 YSTEVEAAVNRVLVNLVLRASVYLSLGFYFDRDDVALGVSHFFRELAEKREAERLLK 68

QY 61 MONORGRALFODLQKPSODEWGTTPDAMKAALVLEKSLNQALLDLHALGSKKADPHLCD 120
DB 69 TONORGRALFODVQKPSODEWGTTLNMEKALALEKLNQALLDLHALGSAKTDHVC 128

QY 121 FLESHFLDEEVKLIKKGMDHLTNIRLVKSKAGLGEYLFERLTLKHD 167
DB 129 FLESHFLDEEVKLIKKGMDHLTNIRLVKSGPQASLGEYLFERLTLKHD 175

RESULT 14
Q6P7T1 PRELIMINARY; PRT; 183 AA.
AC Q6P7T1;
DT 05-JUN-2004 (Tremblrel. 27, Created)
DT 05-JUN-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUN-2004 (Tremblrel. 27, Last annotation update)
```


DE Hypothetical protein.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pituitary gland;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg H., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stepieton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Boeck S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Maitra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pituitary gland;
 RA Strausberg R.;
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Ferritin is an intracellular molecule that stores iron
 CC in a soluble, nontoxic, readily available form. The functional
 CC molecule, which is composed of 24 chains, is roughly spherical and
 CC contains a central cavity into which the polymeric ferric iron
 CC core is deposited (by similarity).
 CC -1- SIMILARITY: Belongs to the ferritin family.
 CC -1- SIMILARITY: Contains 1 ferritin-like diron domain.
 DR EMBL: BC061525; AA061525.1; -;
 DR HSPB; P02791; IAEW.
 DR GO; GO:0005488; P:binding; IEA.
 DR GO; GO:0008199; P:ferric iron binding; IEA.
 DR GO; GO:0006879; P:iron ion homeostasis; IEA.
 DR GO; GO:0006826; P:iron ion transport; IEA.
 DR InterPro: IPR001519; Ferritin.
 DR InterPro: IPR009078; Ferritin/RR_like.
 DR InterPro: IPR008331; Ferritin_Dps.
 DR InterPro: IPR009040; Ferritin_like.
 DR Pfam: PFO0210; Ferritin_1.
 DR ProDom: P000971; Ferritin_1.
 DR PROSITE: PS00540; FERRITIN_1; 1.
 DR PROSITE: PS00204; FERRITIN_2; 1.
 DR PROSITE: PS00905; FERRITIN LIKE; 1.
 DR Hypothetical protein; Iron; Iron storage; Metal-binding.
 KW SEQUENCE 183 AA; 20748 MW; E6AB306251D55106 CRC64;
 SQ

Query Match 84.7%; Score 728; DB 2; Length 183;
 Best Local Similarity 80.6%; Pred. No. 13e-52;
 Matches 141; Conservative 17; Mismatches 9; Indels 8; Gaps 1;

QY 1 YSTEVEAAVNRVLVNYLRASYTYLSIGFPPDRDDVALSEVCHFFPELAEEKEGAEKRLIK 60
 DB 9 YSTEVEAAVNRVLVNYLRASYTYLSIGFPPDRDDVALSEVCHFFPELAEEKEGAEKRLIK 68
 QY 61 MONORGRRLFDOLKRPQODEWGETTPDANKAALIVLEKSNQALLDLHALGSKKADPHLCD 120
 DB 69 LONERGRRLFDVQKRPQODEWGETTPDANKAALIVLEKSNQALLDLHALGSKKADPHLCD 128
 QY 121 FLESHFLDEVKLIKMGHNLINQILV-----KSRAGGEVYFERTLTAKHD 167
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

DB 129 FLESHFLDEVKLIKMGHNLINLRVAGPQPAQTGAQASLGSEYFERTLTAKHD 183
 RESULT 15
 ID FRIL_RAT STANDARD; PRT; 182 AA.
 AC P02793;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ferritin light chain (ferritin L subunit).
 GN Name=Fcl;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=87222340; PubMed=3584116;
 RA Leibold E.A., Munro H.N.;
 RT "Characterization and evolution of the expressed rat ferritin light
 RT subunit gene and its pseudogene family. Conservation of sequences
 RT within noncoding regions of ferritin genes.";
 RL J. Biol. Chem. 262:7335-7341 (1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=84162134; PubMed=6546756;
 RA Leibold E.A., Aziz N., Brown A.J.P., Munro H.N.;
 RT "Conservation in rat liver of light and heavy subunit sequences of
 RT mammalian ferritin. Presence of unique octapeptide in the light
 RT subunit.";
 RL J. Biol. Chem. 259:4327-4334 (1984).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92210224; PubMed=1555892;
 RA Denis M.G.;
 RT "Isolation of cDNA clones corresponding to genes differentially
 RT expressed in two colon-carcinoma cell lines differing by their
 RT tumorigenicity.";
 RL Int. J. Cancer 50:930-936 (1992).
 CC -1- FUNCTION: Ferritin is an intracellular molecule that stores iron
 CC in a soluble, nontoxic, readily available form. The functional
 CC molecule, which is composed of 24 chains, is roughly spherical and
 CC contains a central cavity into which the polymeric ferric iron
 CC core is deposited.
 CC -1- TISSUE SPECIFICITY: In rat liver, the light chain is the major
 CC chain.
 CC -1- DOMAIN: The rat light chain has an octapeptide insertion after
 CC residue 158 compared with other light chains.
 CC -1- MISCELLANEOUS: There are two types of ferritin subunits: L (light)
 CC chain and H (heavy) chain. The major chain can be light or heavy,
 CC depending on the species and tissue type.
 CC -1- SIMILARITY: Belongs to the ferritin family.
 CC -1- SIMILARITY: Contains 1 ferritin-like diron domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC at the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sdb.ch/announce/>
 CC or send an email to license@sdb.ch).
 CC -----
 DR EMBL: K01930; AAA41154.1; -;
 DR EMBL: J02741; AAA41155.1; -;
 DR EMBL: L01122; AAA41152.1; -;
 DR PIR: A29575; FERTL.
 DR PIR: I54774; I54774.
 DR HSPB; P29391; ILB3.
 DR InterPro: IPR001519; Ferritin.
 DR InterPro: IPR009078; Ferritin/RR_like.

DR	InterPro: IPRO08331, Ferritin Dps.		
DR	InterPro: IPRO09040, Ferritin_Like.		
DR	Pfam: PF00210, Ferritin_1.		
DR	ProDom: PD000971, Ferritin_1.		
DR	PROSITE: PS00540, FERRITIN_1, 1.		
DR	PROSITE: PS00204, FERRITIN_2, 1.		
DR	PROSITE: PS01905, FERRITIN_Like, 1.		
KW	Iron; Iron storage; Metal-Binding.		
FT	INIT MET	0	0
FT	DOMAIN	6	155
FT	METAL	53	53
FT	METAL	56	56
FT	METAL	57	57
FT	METAL	60	60
FT	METAL	63	63
FT	CONFLICT	97	97
FT	CONFLICT	120	121
FT	CONFLICT	125	125
FT	CONFLICT	154	154
FT	CONFLICT	155	155
FO	SEQUENCE	152 AA; 20674 MW; 3D1DEACE508655B CRC64	

Query Match	84.4%;	Score 726;	DB 1;	Length 182;
Best Local Similarity	80.6%;	Pred. No. 1.9e-52;		
Matches 141;	Conservative 17;	Mismatches 9;	Indels 8;	Gaps 1;

QY	1	YSYSEVEAANRVNLNLTLPASITYYLSLGFPEBDDVALGCVGHPPRELAEBEERBEAELTK	60
		
Db	8	YSYSEVEAANRVNLNLTLPASITYYLSLGFPEBDDVALGCVGHPPRELAEBEERBEAELTK	67
		
QY	61	MONORGRALFOLOLQPSODENGTTPDANKAIYIEKSLNQLDHALGSKKADPHLCD	120
		
Db	68	LONERGRALFOVQPSODENGKTLAEAMEALALEKLNQLDLHALGSGARDPHLCD	127
		
QY	121	FLSHFLDEEVKIKKMGHLLTNLQRLV-----KSKAGIGEYLFERLLTKKD	167
		
Db	128	FLSHFLDEEVKIKKMGHLLTNLRVQSPCPAQGVAAQSLGELFERLLTKKD	182

Search completed: August 22, 2005, 09:10:08
Job time : 174 secs